Fig. 1

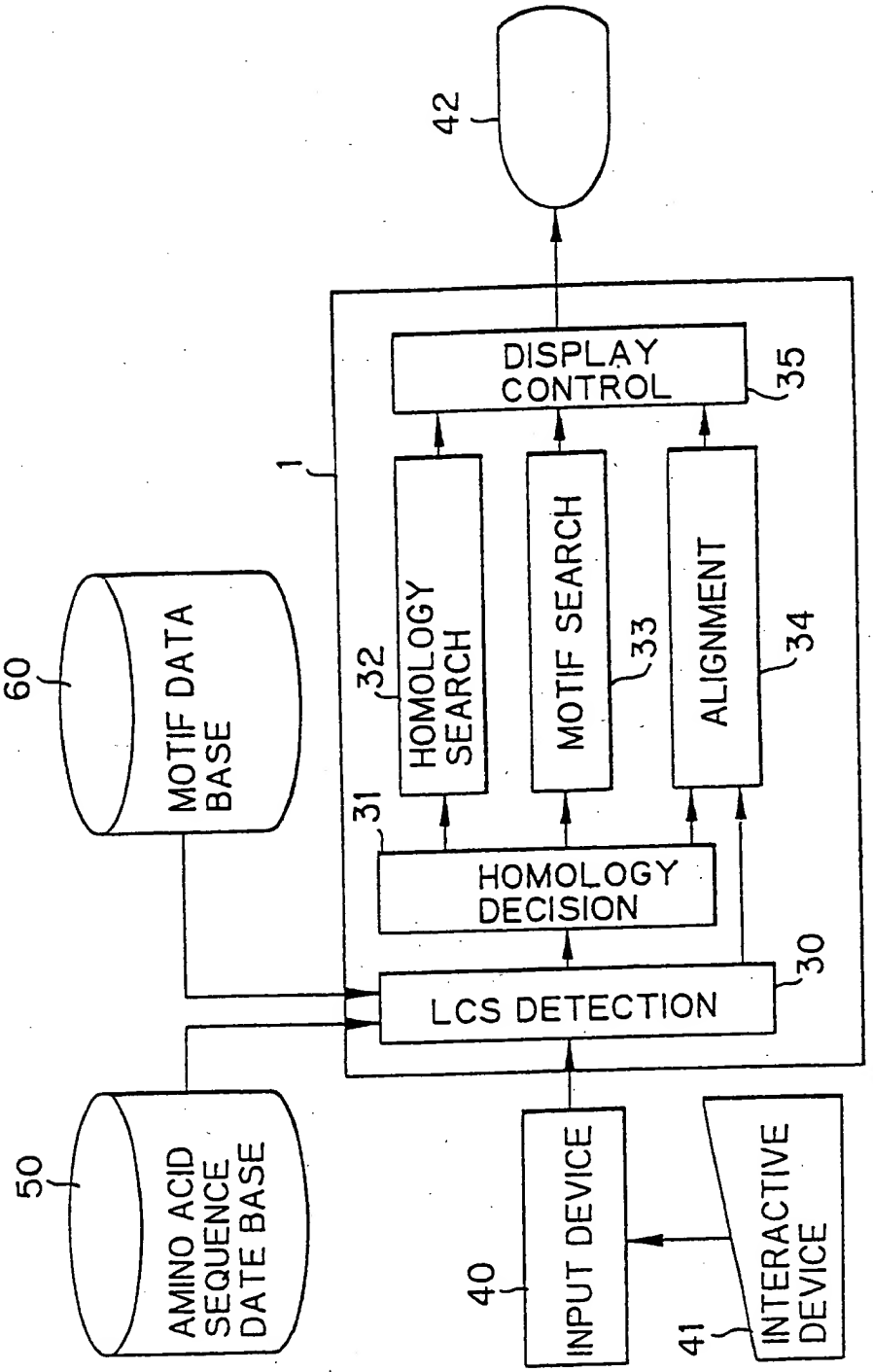


Fig. 2

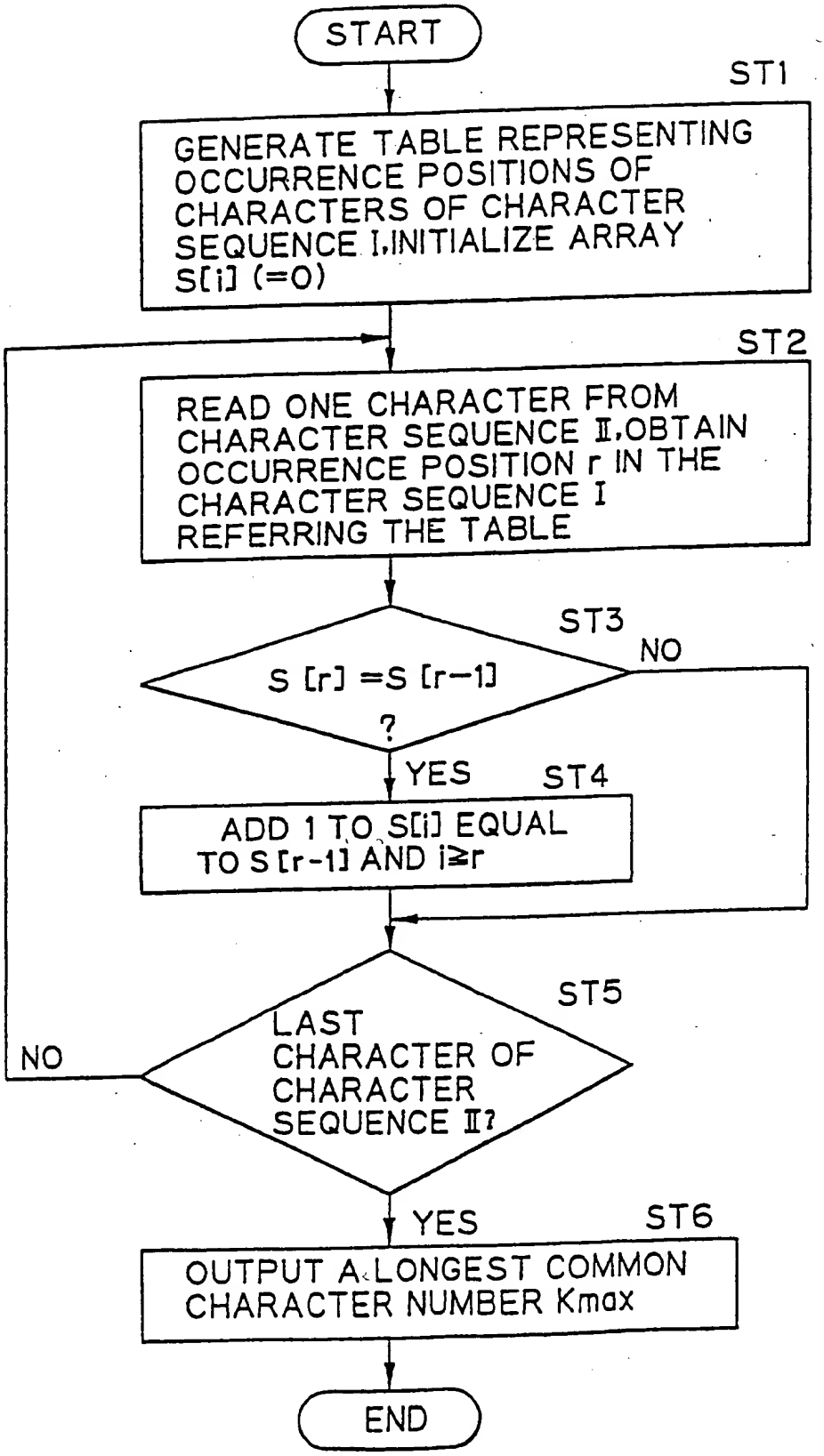


Fig. 3

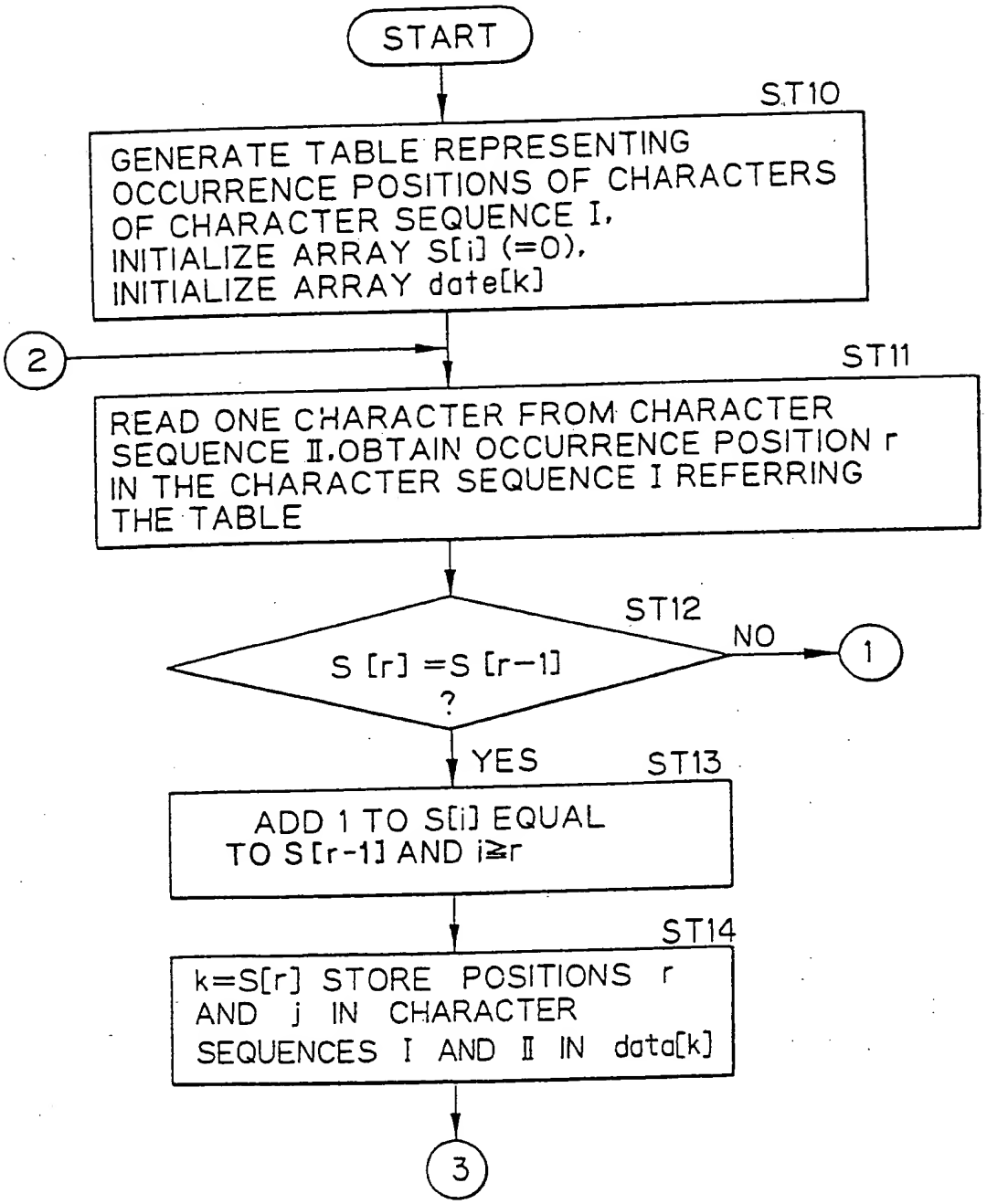


Fig. 4

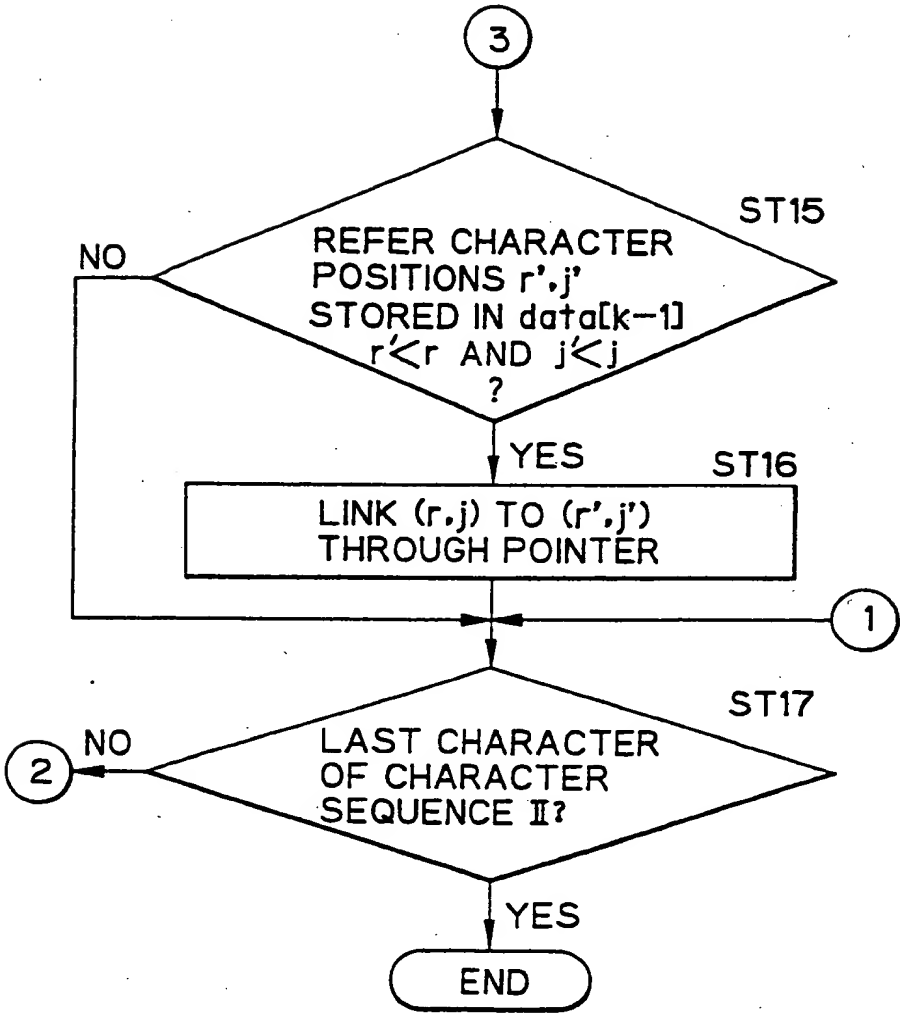


Fig. 5

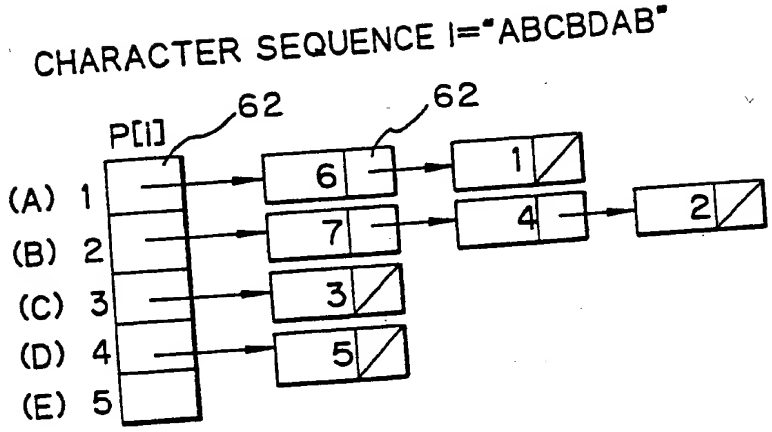


Fig. 6

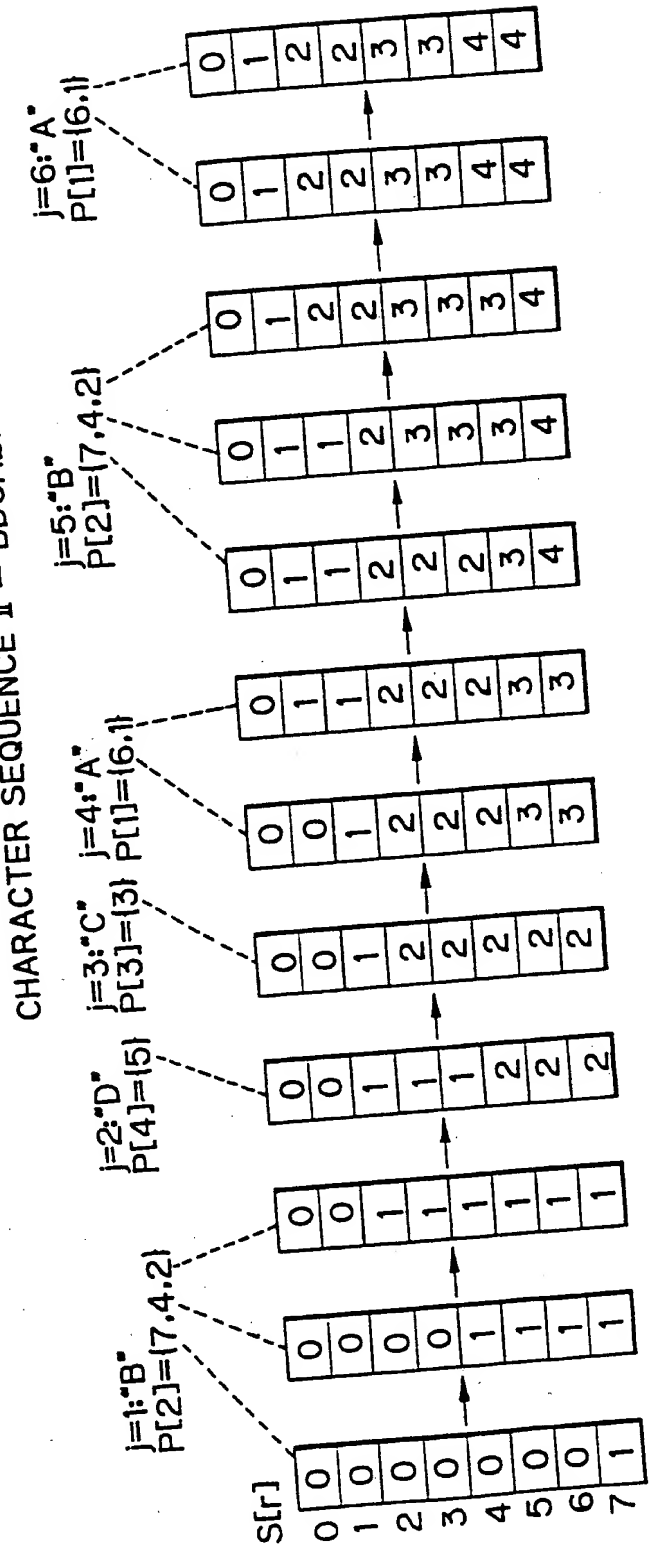


Fig. 7

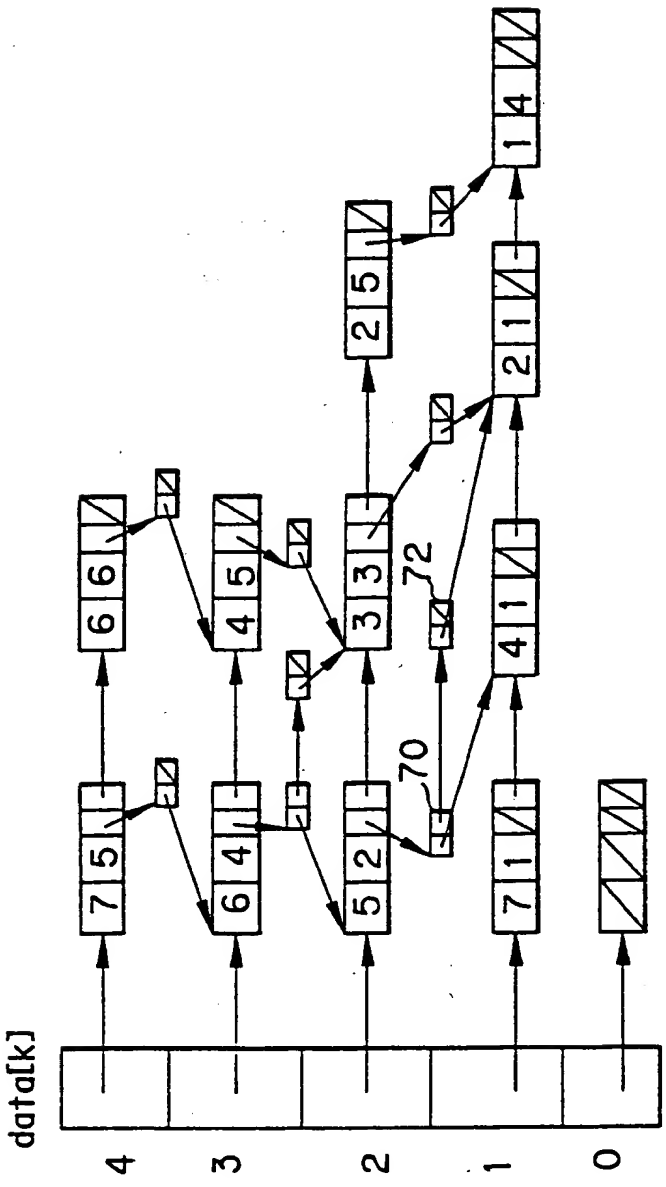


Fig. 8

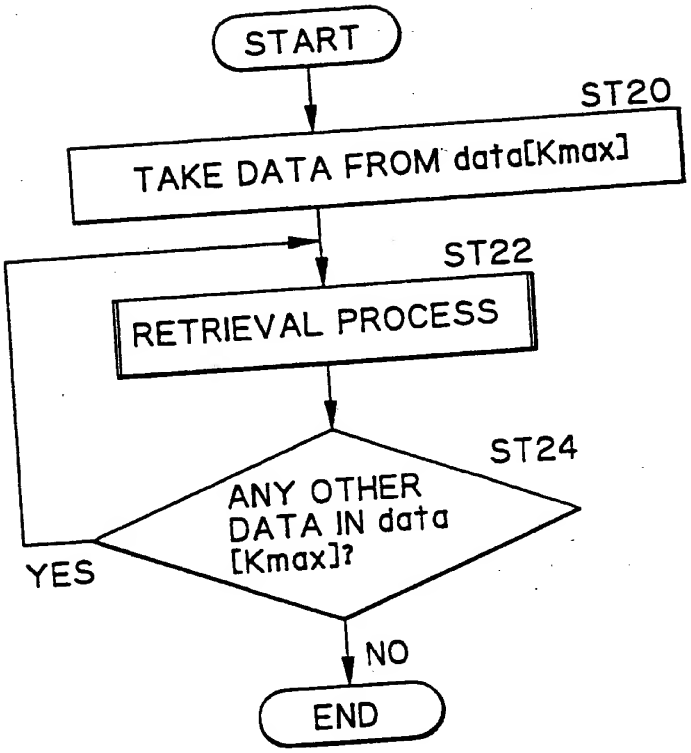


Fig. 9

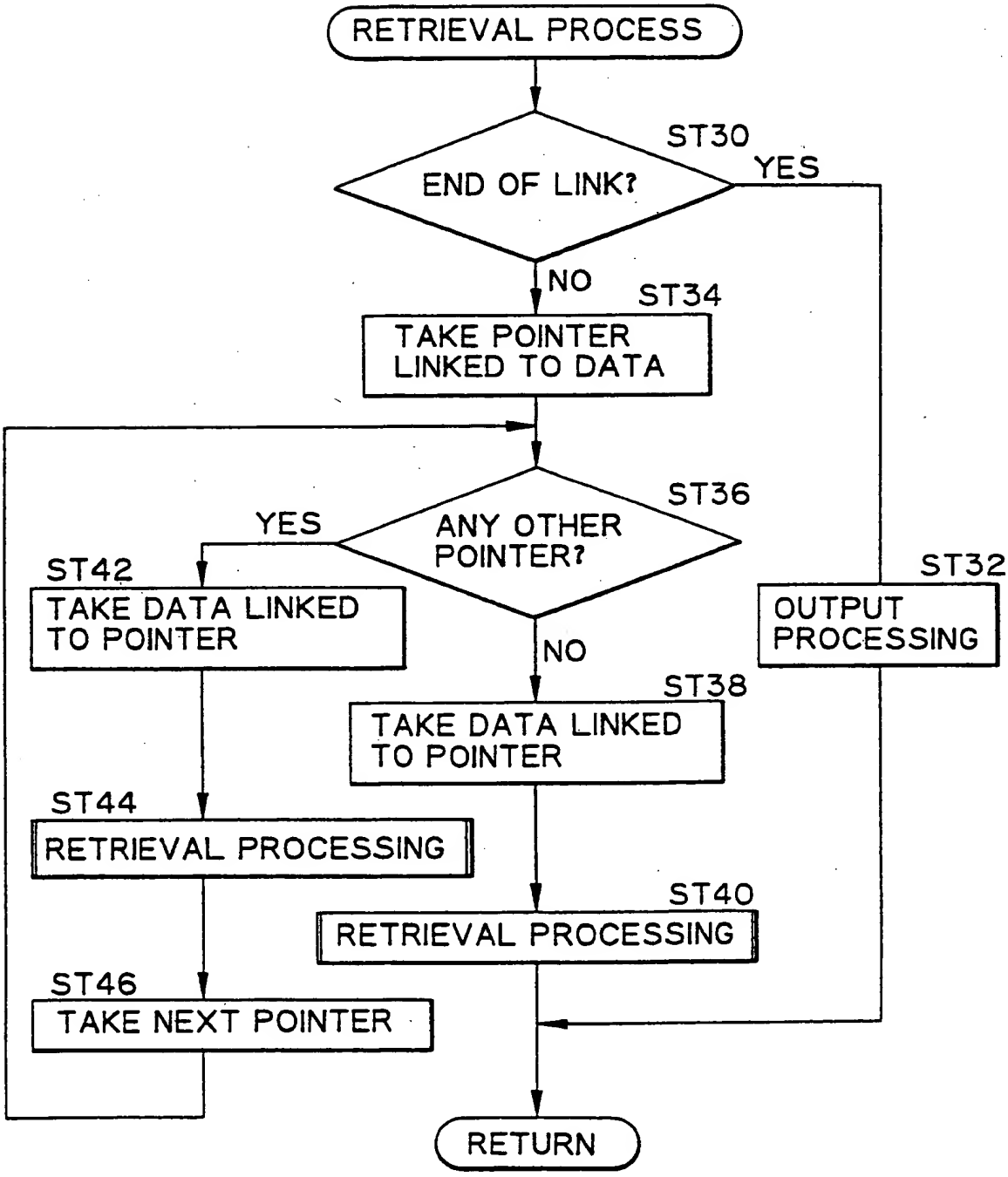


Fig. 10

human : GDVEKGKKIFIMKCSQCHTVEGGKHKTGPNLHGLFGRK SEQ ID NO: 1
bacterium : EGDAAAGEKVSKKCLACHTFDQGGANKVGPNPNLFGVF SEQ ID NO: 2

LCS : GD(x3.3)G(x0.1)K(x0.2)K(x4.0)KC(x2.2)CHT(x3.3)GG(x2.2)K
GD(x1.4)E(x0.2)K(x0.2)K(x0.4)KC(x2.2)CHT(x3.3)GG(x2.2)K

homology : 47%

Fig. 11

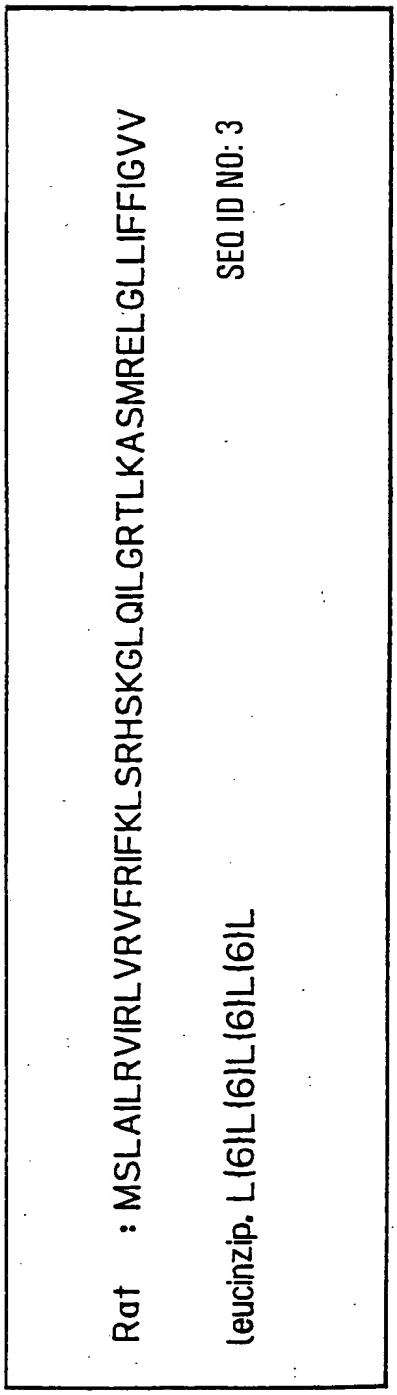


Fig. 12

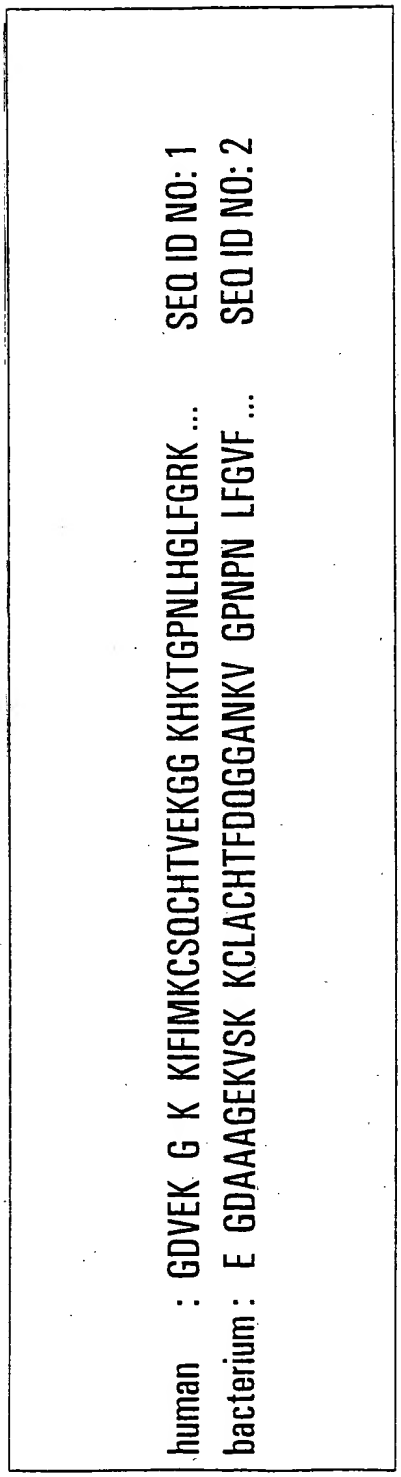
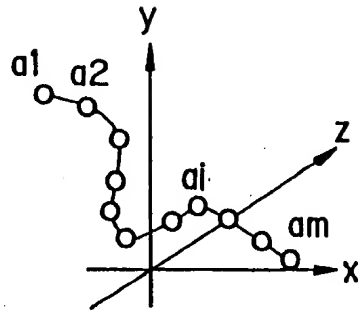
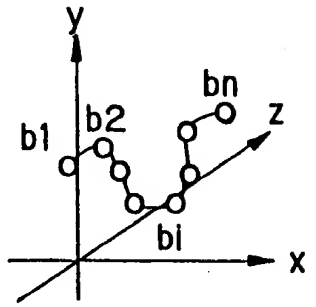


Fig. 13 A



A={a1,a2....ai....am}

Fig. 13 B



B={b1,b2....bj....bn}

Fig. 13C

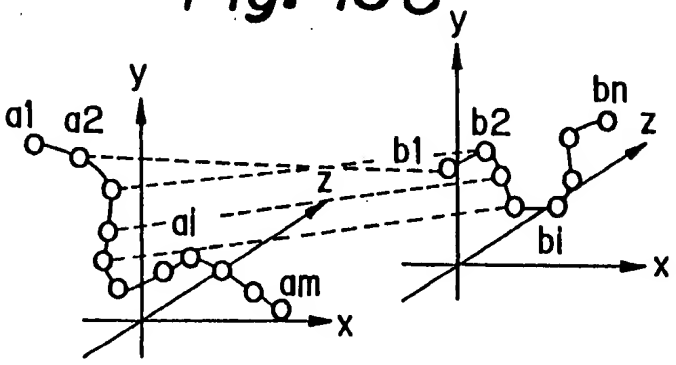


Fig. 13 D

$$r.m.s.d = \frac{\sqrt{\sum_{k=1}^{n} w_k (Ub_k - a_k)^2}}{n}$$

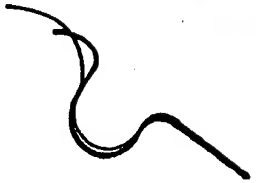


Fig. 14 A

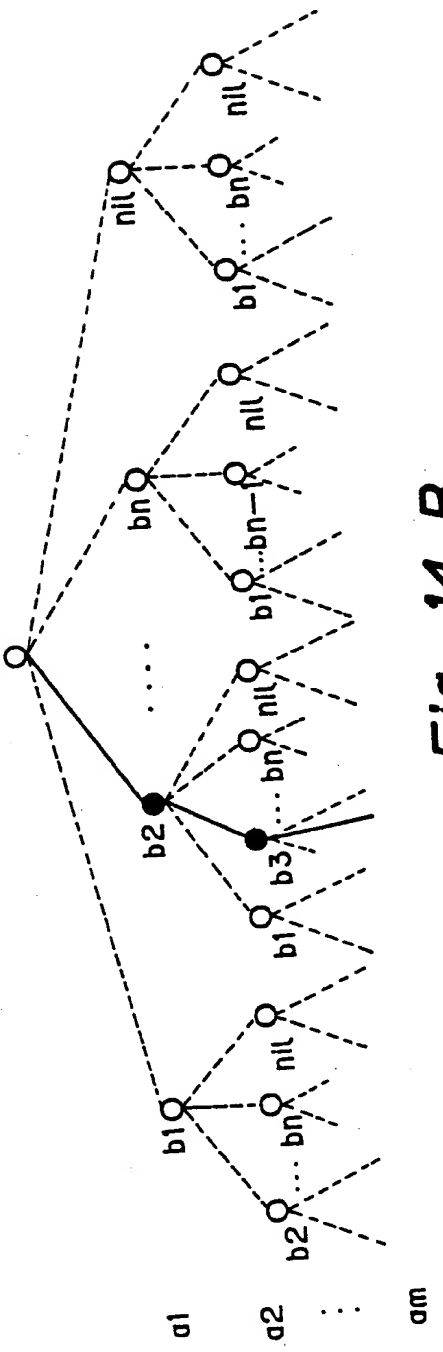


Fig. 14 B

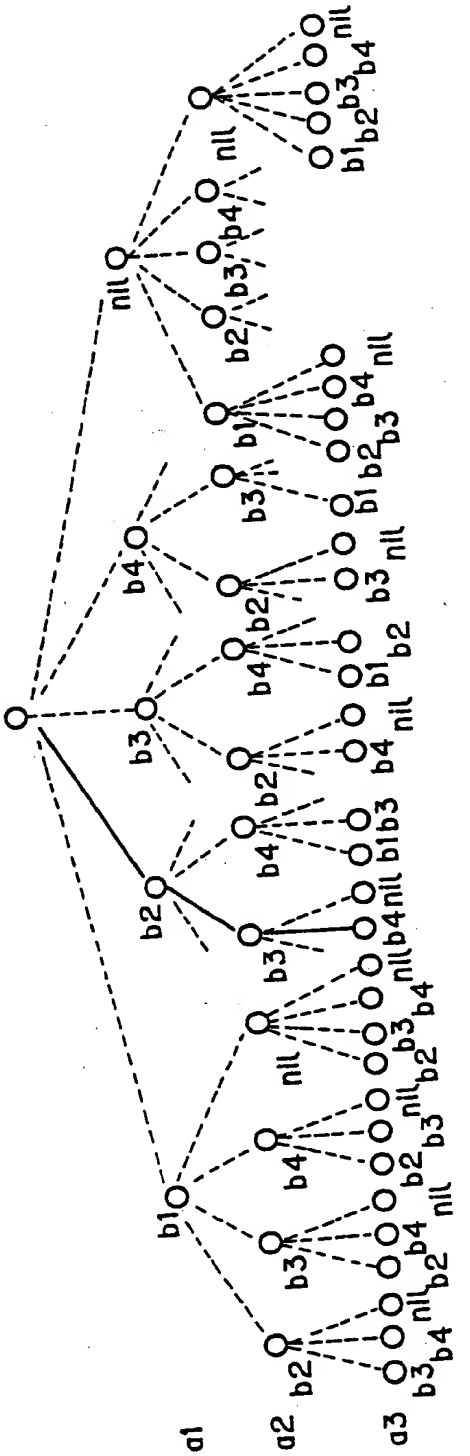


Fig. 15

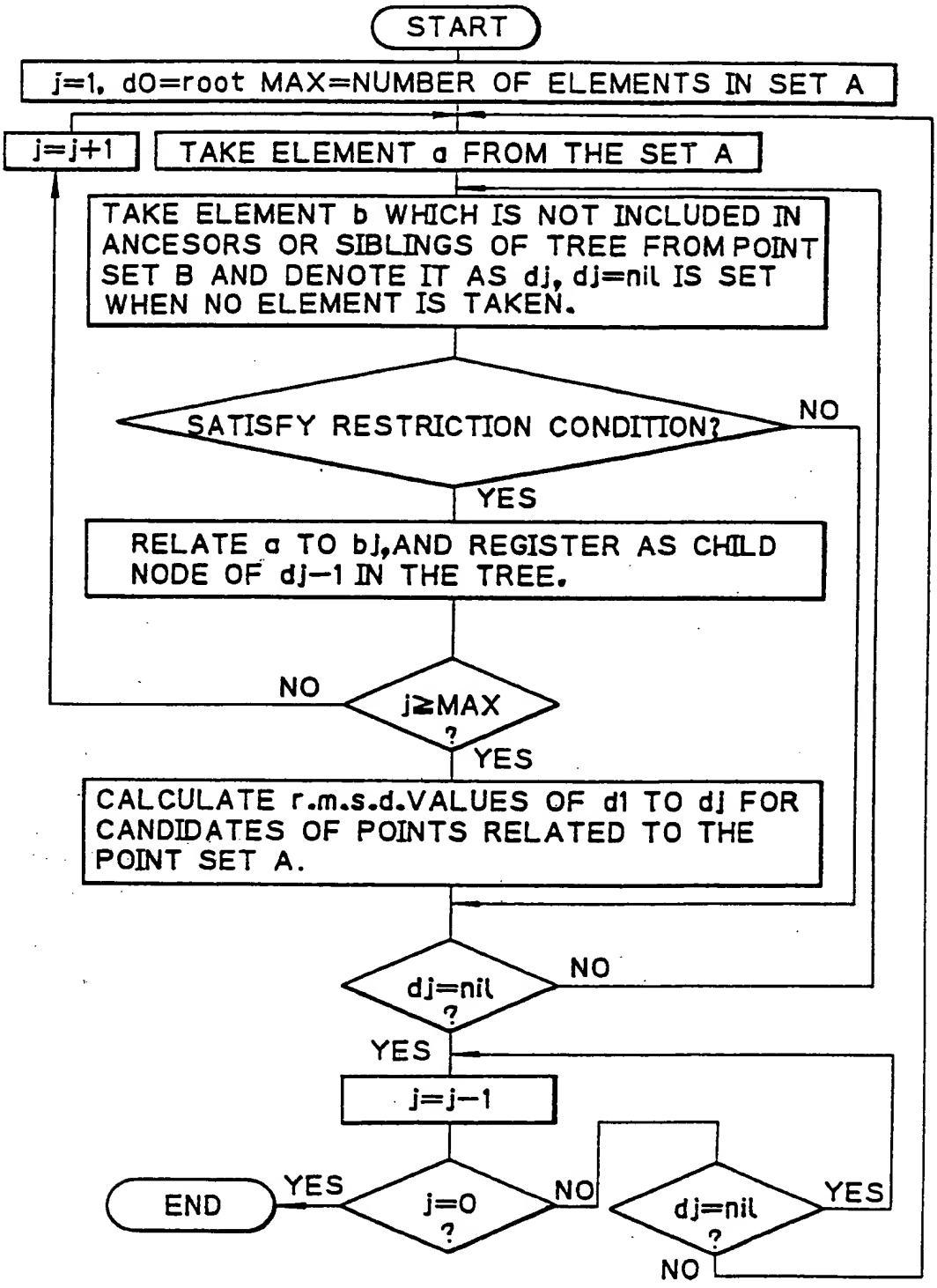


Fig. 16 A

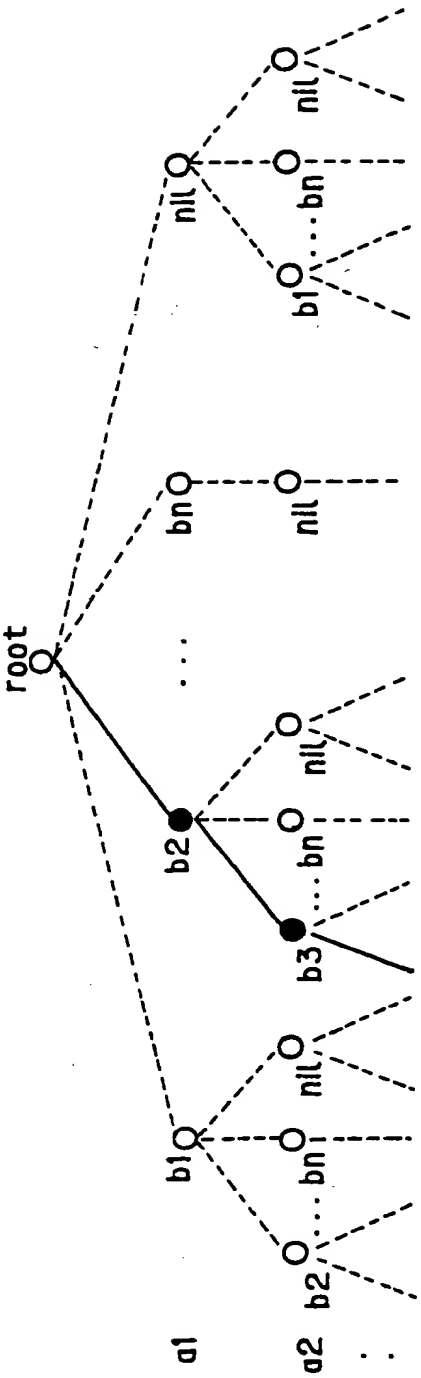


Fig. 16 B

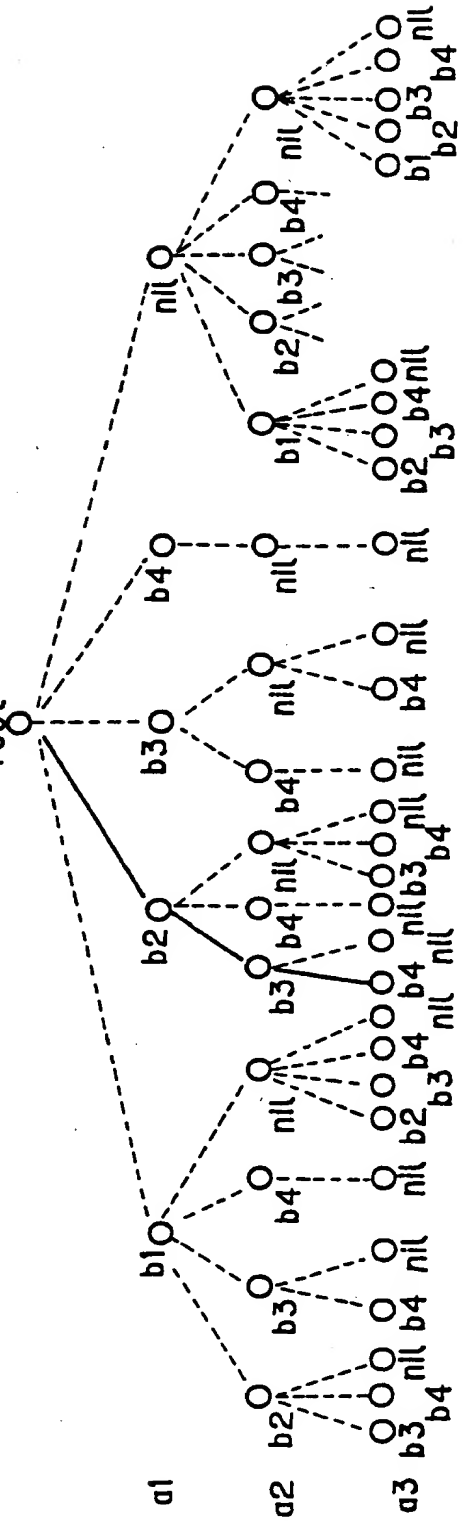


Fig. 17

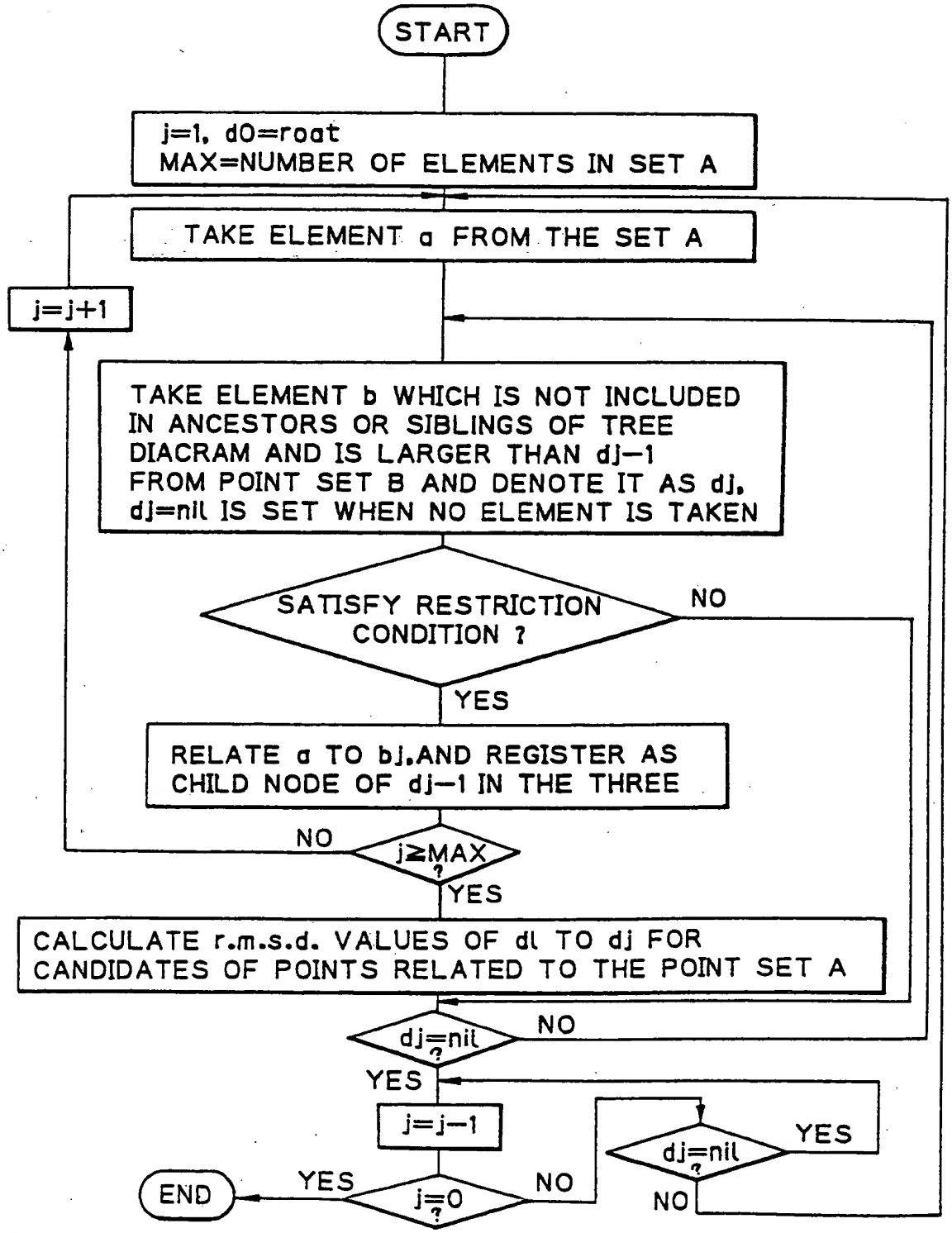


Fig. 18

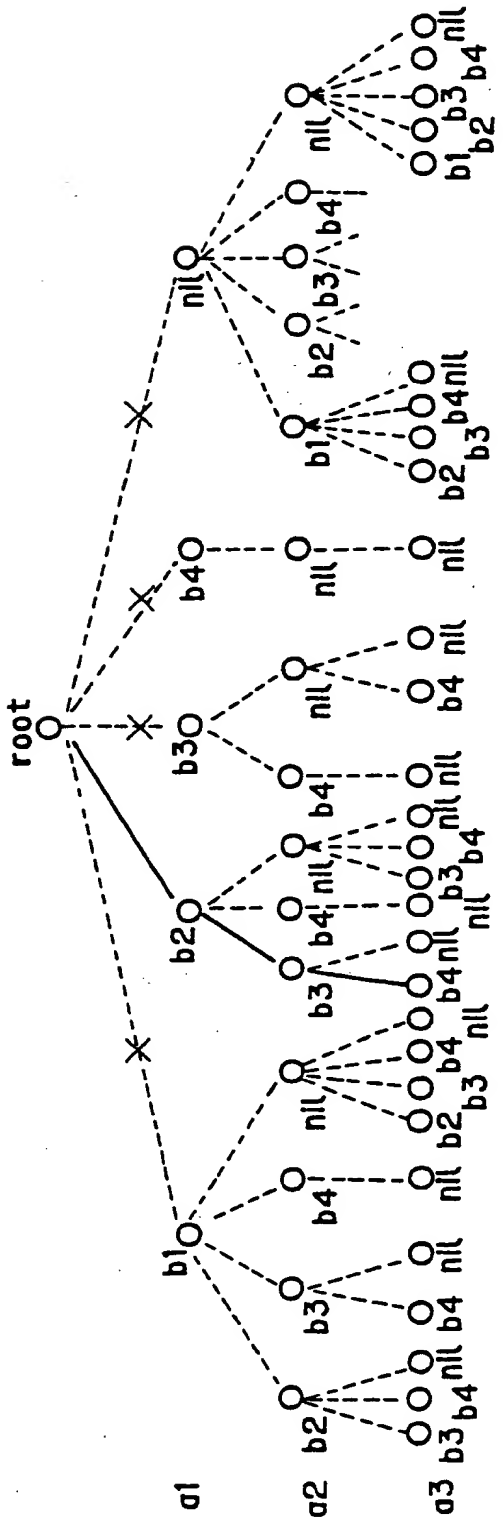


Fig. 19 B

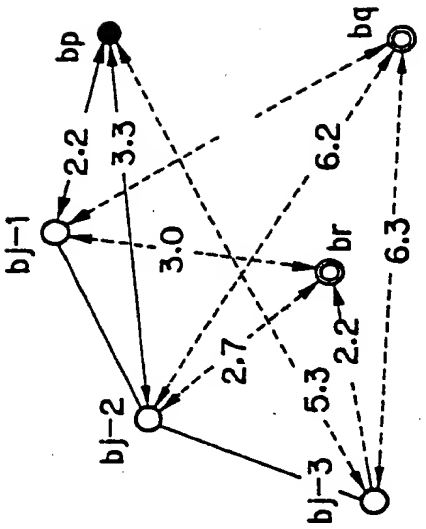


Fig. 20 B

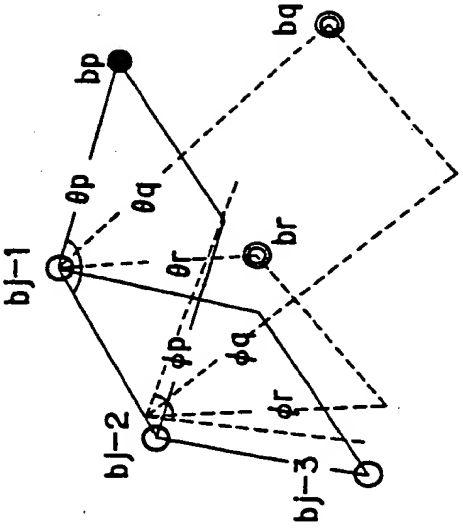


Fig. 19 A

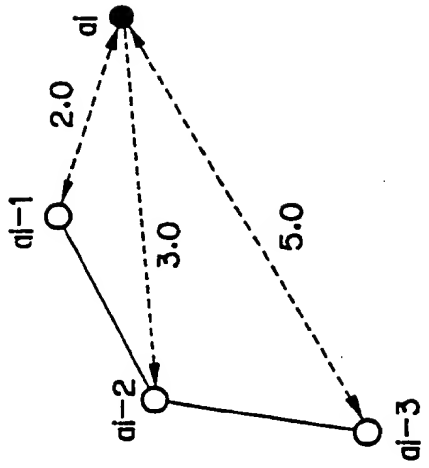


Fig. 20 A

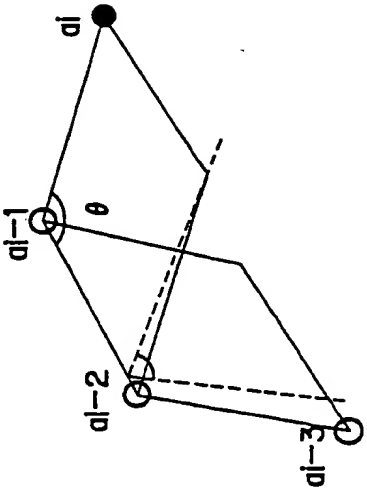
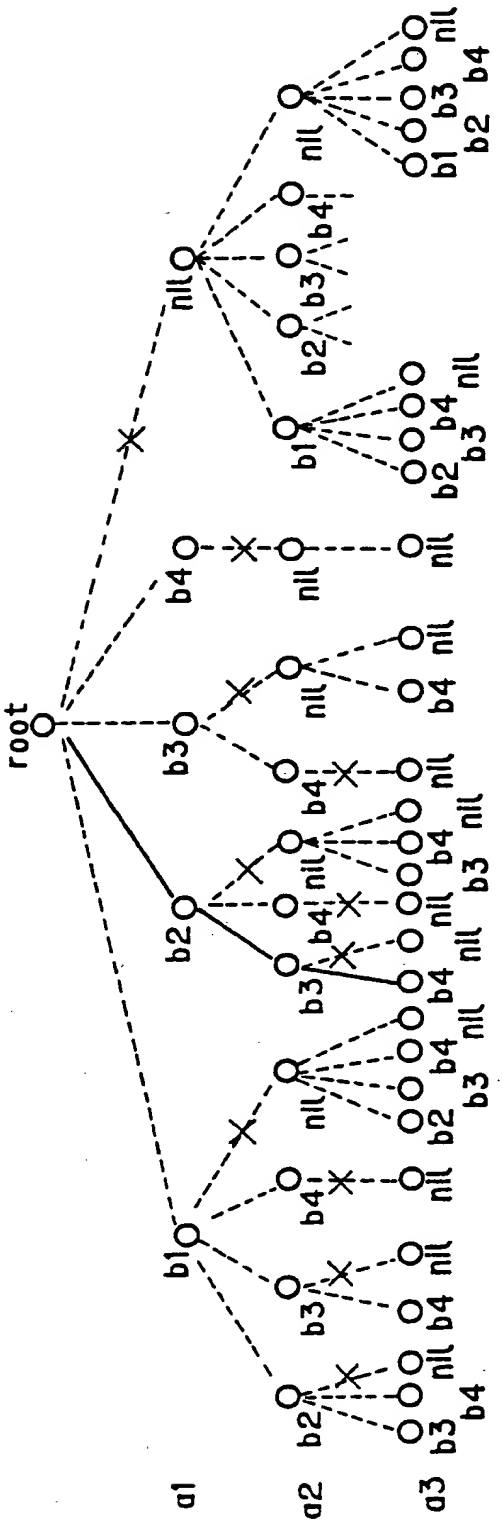


Fig. 21



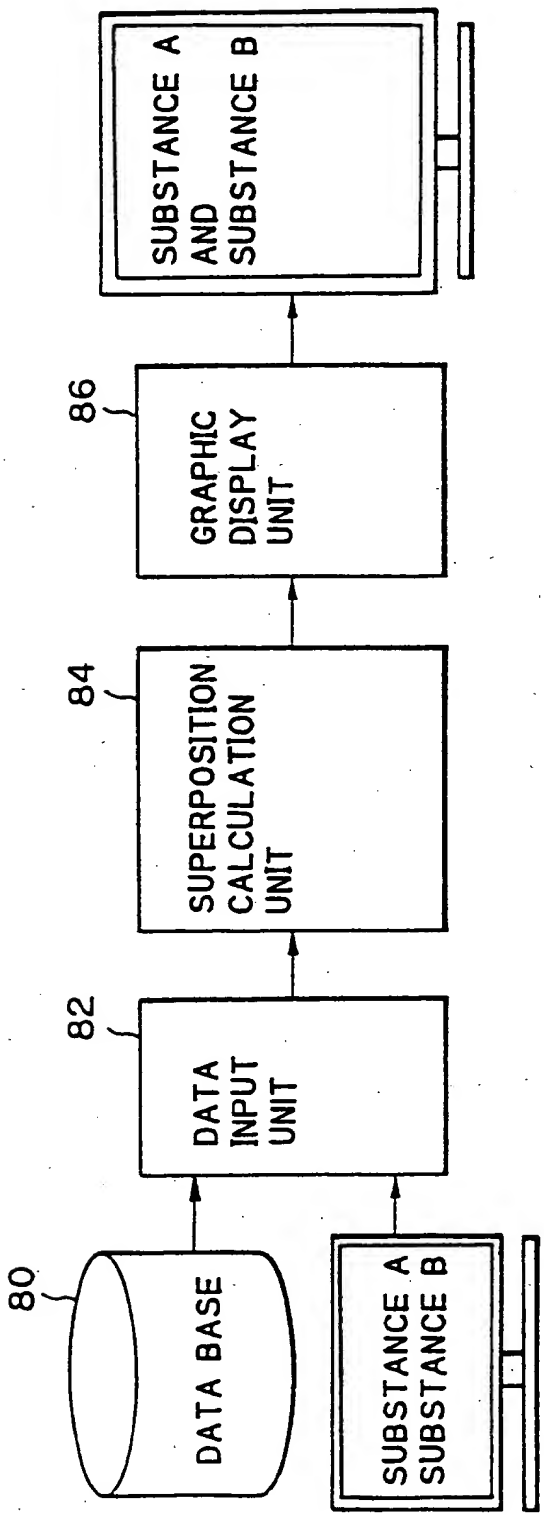


Fig. 22

Fig. 23 A

1	T E E Q I A E F K E	A F S L F D K D G D
21	G T I T T K E L G T	V M R S L G Q N P T
41	E A E L Q D M I N E	V D A D G N G T I D
61	F P E F L T M M A R	K M K D T D S E E E
81	I R E A F R V F D K	D G N G Y I S A A E
101	L R H V M T N L G E	K L T D E E V D E M
121	I R E A N I D G D G	Q V N Y E E F V Q M
141	M T A	

AMINO ACID SEQUENCE OF CALMODULIN (EXCERPT FROM PDB) SEQ ID NO: 4

Fig. 23 B

1	A M D Q Q A E A R A	F L S E E M I A E F
21	K A A F D M F D A D	G G G D I S T K E L
41	G T V M R M L G Q N	P T K E E L D A I I
61	E E V D E D G S G T	I D F E E F L V M
81	V R Q M K E D A K G	K S E E E L A D C F
101	R I F D K N A D G F	I D I E E L G E I L
121	R A T G E H V T E E	D I E D L M K D S D
141	K N N D G R I D F D	E F L K M M E G V Q
161		

AMINO ACID SEQUENCE OF TROPONIN C (EXCERPT FROM PDB) SEQ ID NO: 5

Fig. 24 B

TROPONIN C

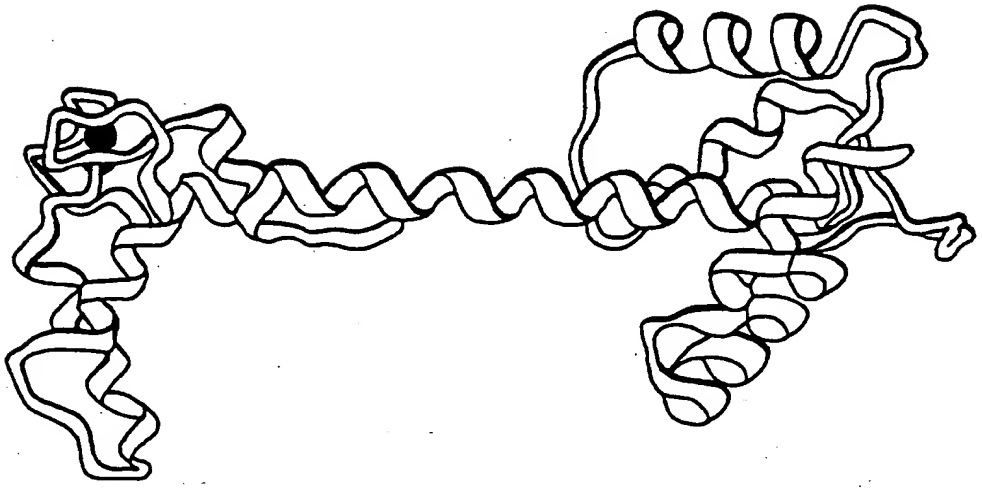


Fig. 24 A

CALMODULIN

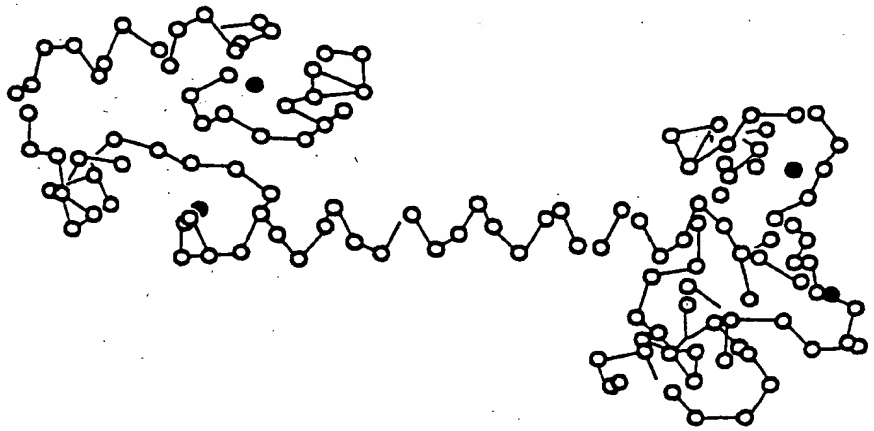


Fig. 25

Probe site = 81-108 in Calmodulin

96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	SEQ ID NO: 6
L	A	D	C	F	R	I	F	D	K	N	A	D	G	F	< target >
I	R	E	A	F	R	V	F	D	K	D	G	N	G	Y	< probe >

111	112	113	114	115	116	117	118	119	120	121	122	123	SEQ ID NO: 7
I	D	I	E	E	L	G	E	I	L	R	A	T	SEQ ID NO: 6 < target >
I	S	A	A	E	L	R	H	V	M	T	N	L	< probe > SEQ ID NO: 7

rmsd = 0.567034

Fig. 26

Probe site = 81-108 and 117-143 in Calmodulin

96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	SEQ ID NO: 6
L	A	D	C	F	R	I	F	D	K	N	A	D	G	F	< target >
I	R	E	A	F	R	V	F	D	K	D	G	N	G	Y	< probe > SEQ ID NO: 7
111	112	113	114	115	116	117	118	119	120	121	122	123			
	I	D	I	E	E	L	G	E	I	L	R	A	T		< target > SEQ ID NO. 6
	I	S	A	A	E	L	R	H	V	M	T	N	L		< probe > SEQ ID NO: 7
132	133	134	135	136	137	138	139	140	141	142	143	144	145		SEQ ID NO: 8
	I	E	D	L	M	K	D	S	D	K	N	N	D	G	< target >
	V	D	E	M	I	R	E	A	N	I	D	G	D	G	< probe > SEQ ID NO: 9
146	147	148	149	150	151	152	153	154	155	156	157	158			
	R	I	D	F	D	E	F	L	K	M	M	E	G		< target > SEQ ID NO: 8
	Q	V	N	Y	E	E	F	V	Q	M	M	T	A		< probe > SEQ ID NO: 9

rmsd = 0.823665

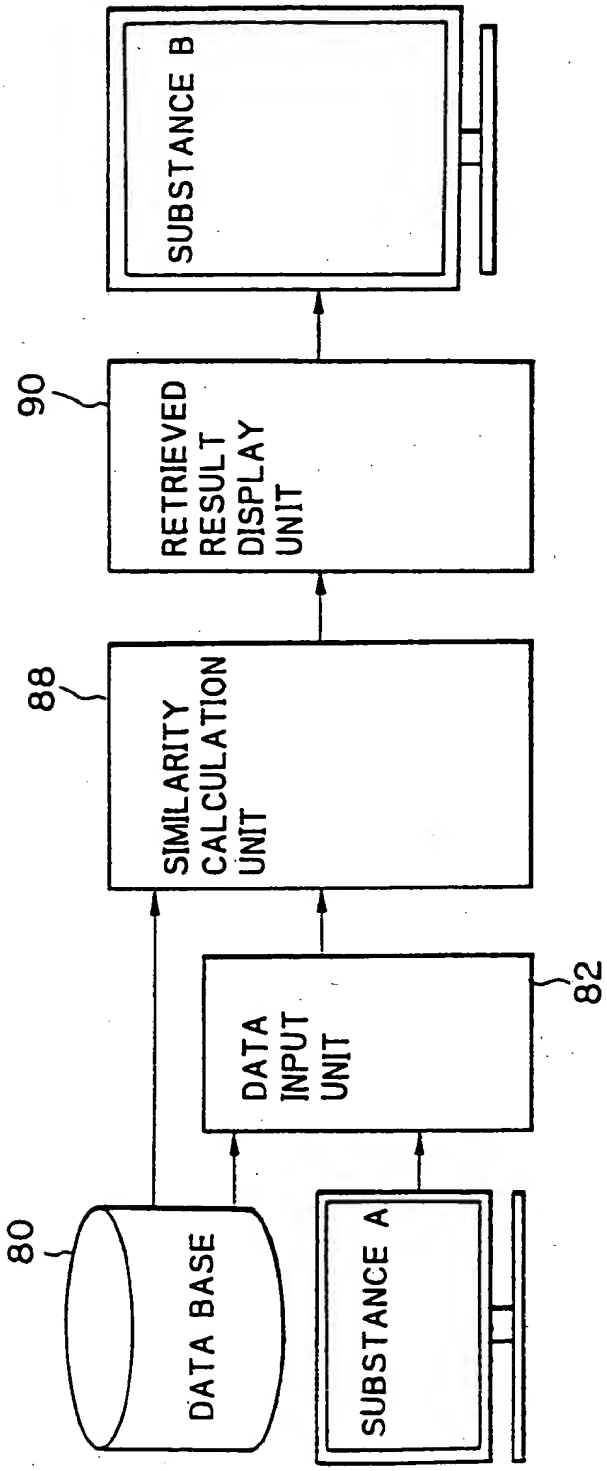


Fig. 27

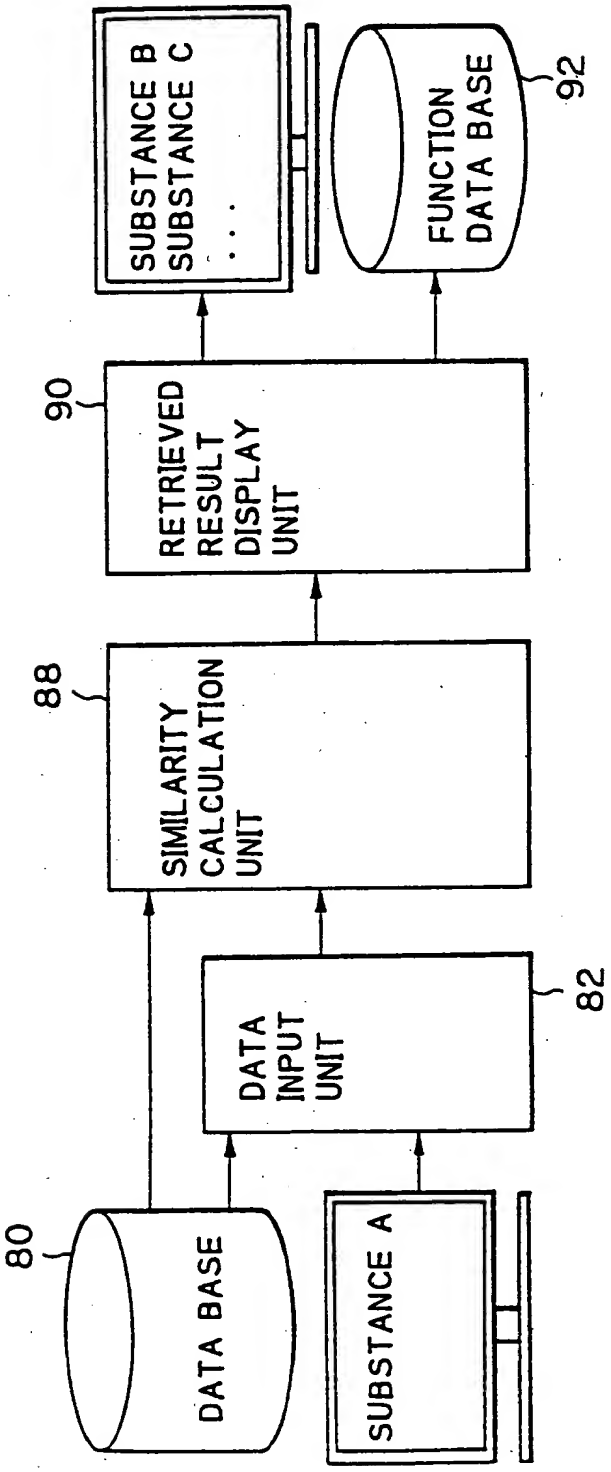


Fig. 28

Fig. 29

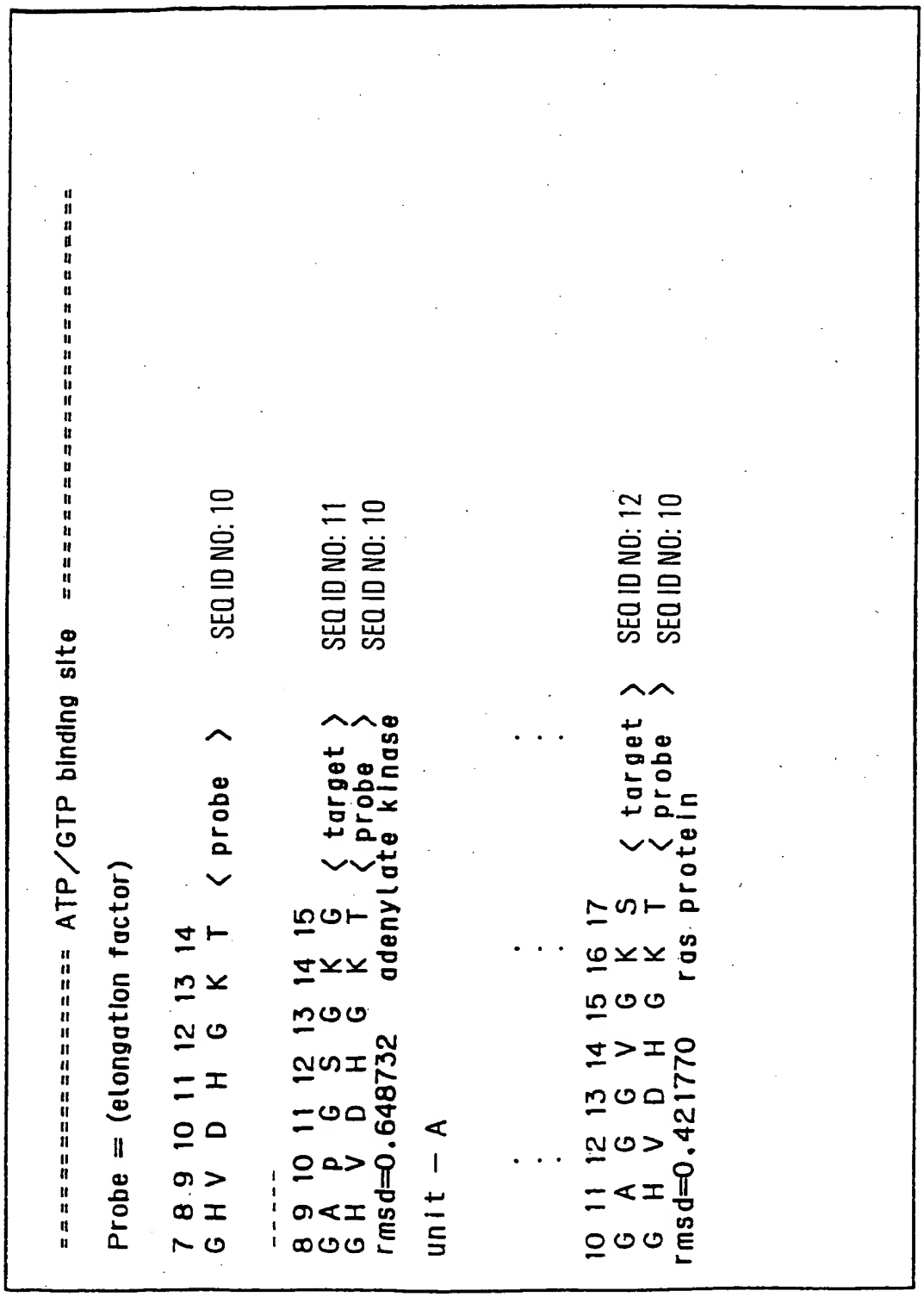


Fig. 30

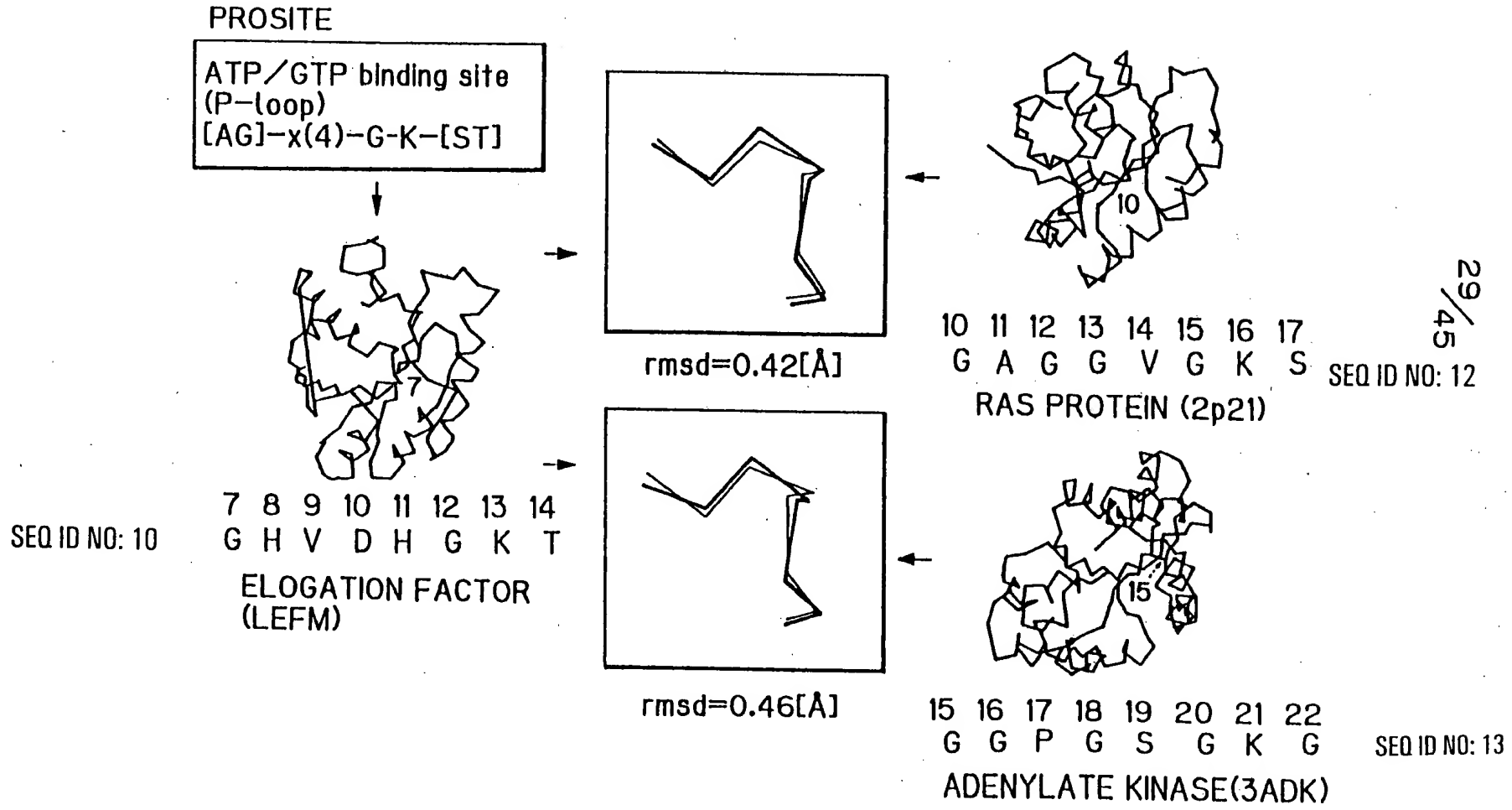


Fig. 31

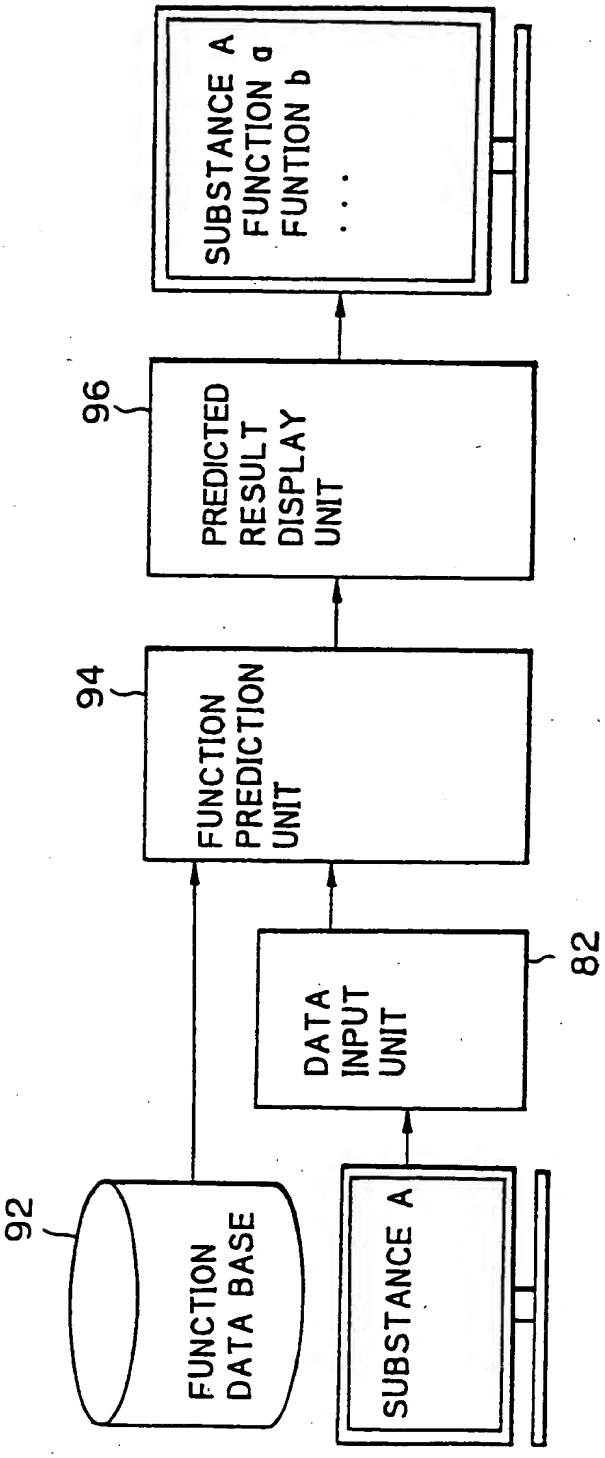
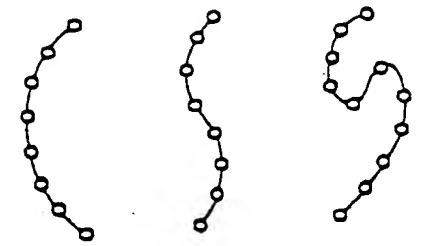
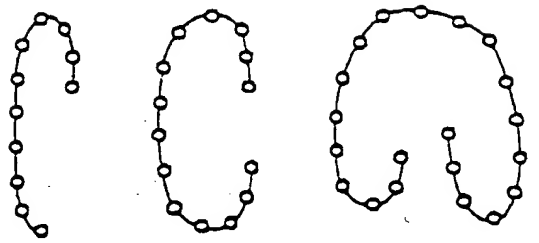


Fig. 32 A



LINEAR STRUCTURE

Fig. 32 B

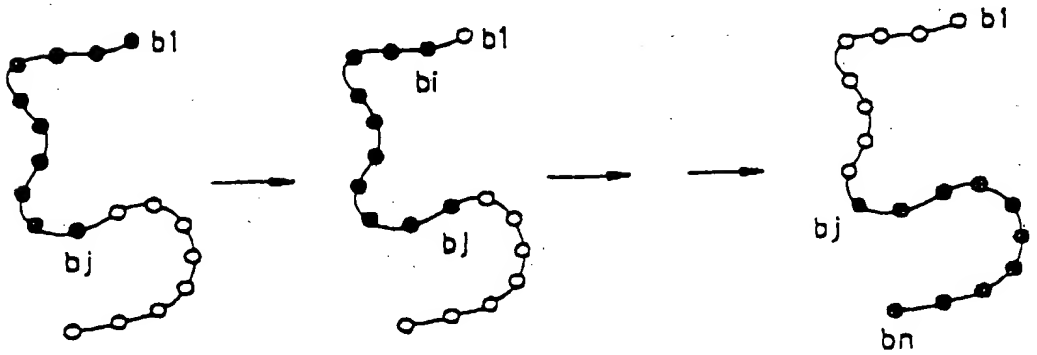


NON-LINEAR STRUCTURE

Fig. 33

WHEN f(x)=2x

A={a1.....am}



B={b1.....bi.....bj.....bn}

Fig. 34

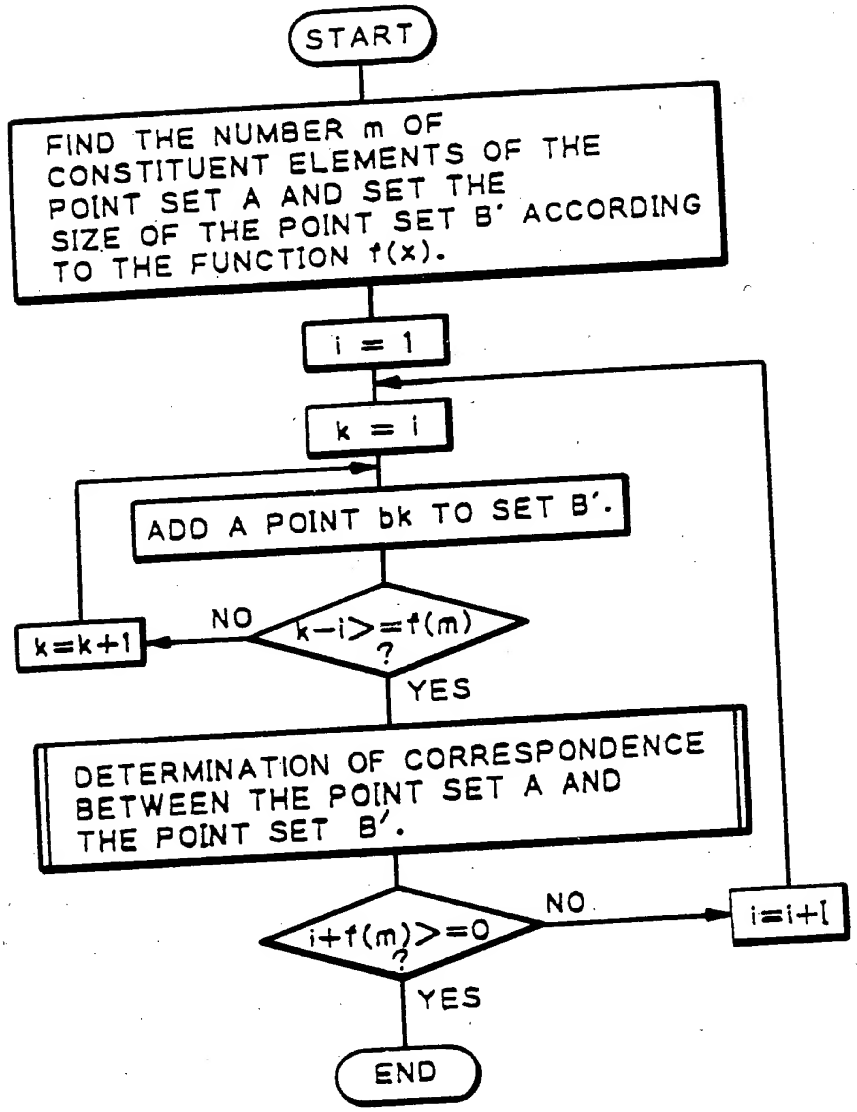
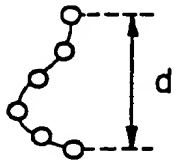
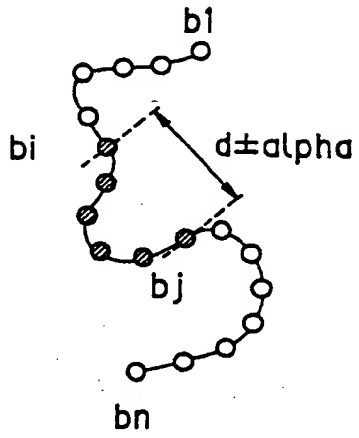


Fig. 35 A



A={a1.a2.....am}

Fig. 35 B



B={b1.....bi.....bj.....bn}

Fig. 36

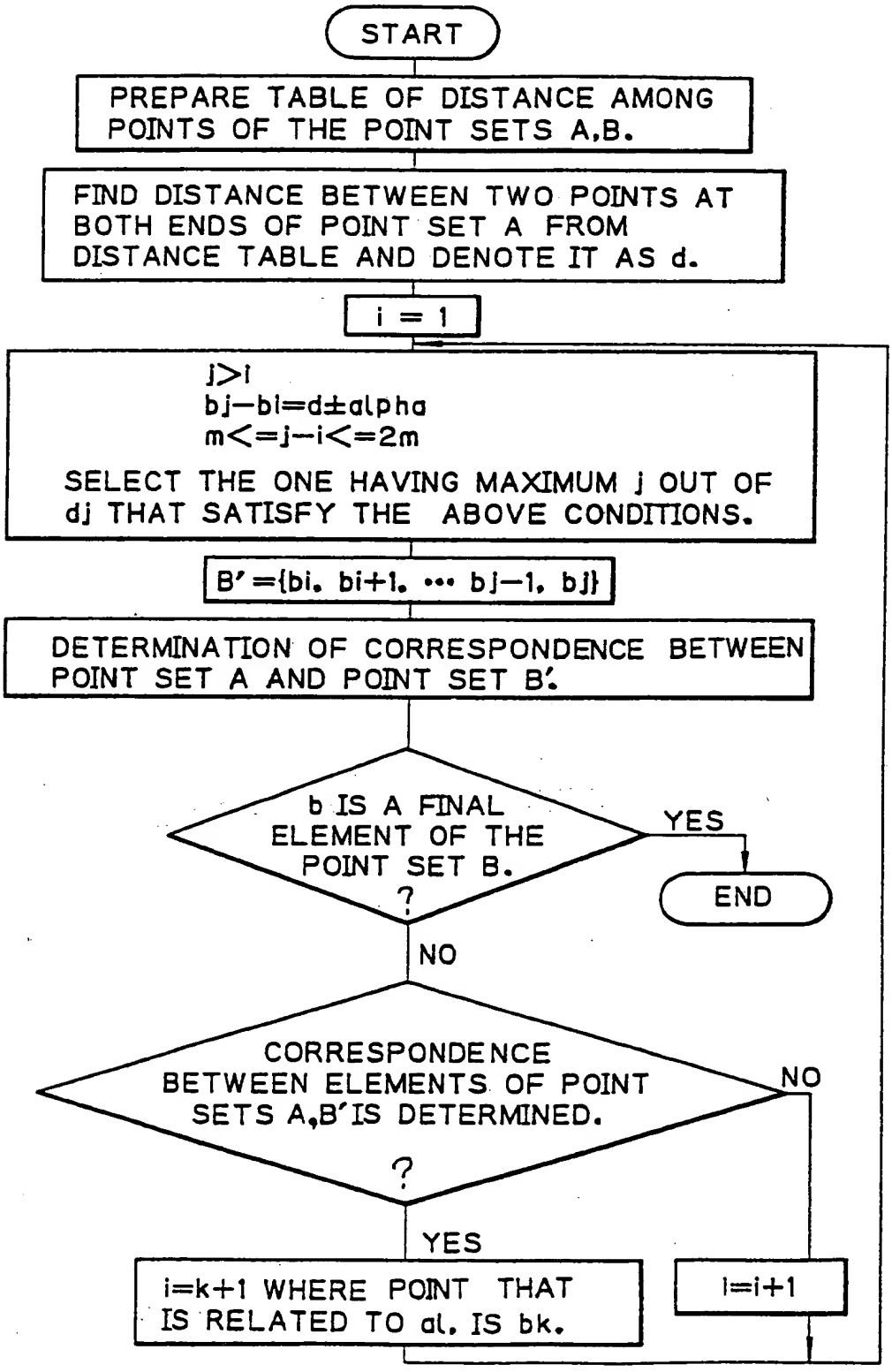


Fig. 37

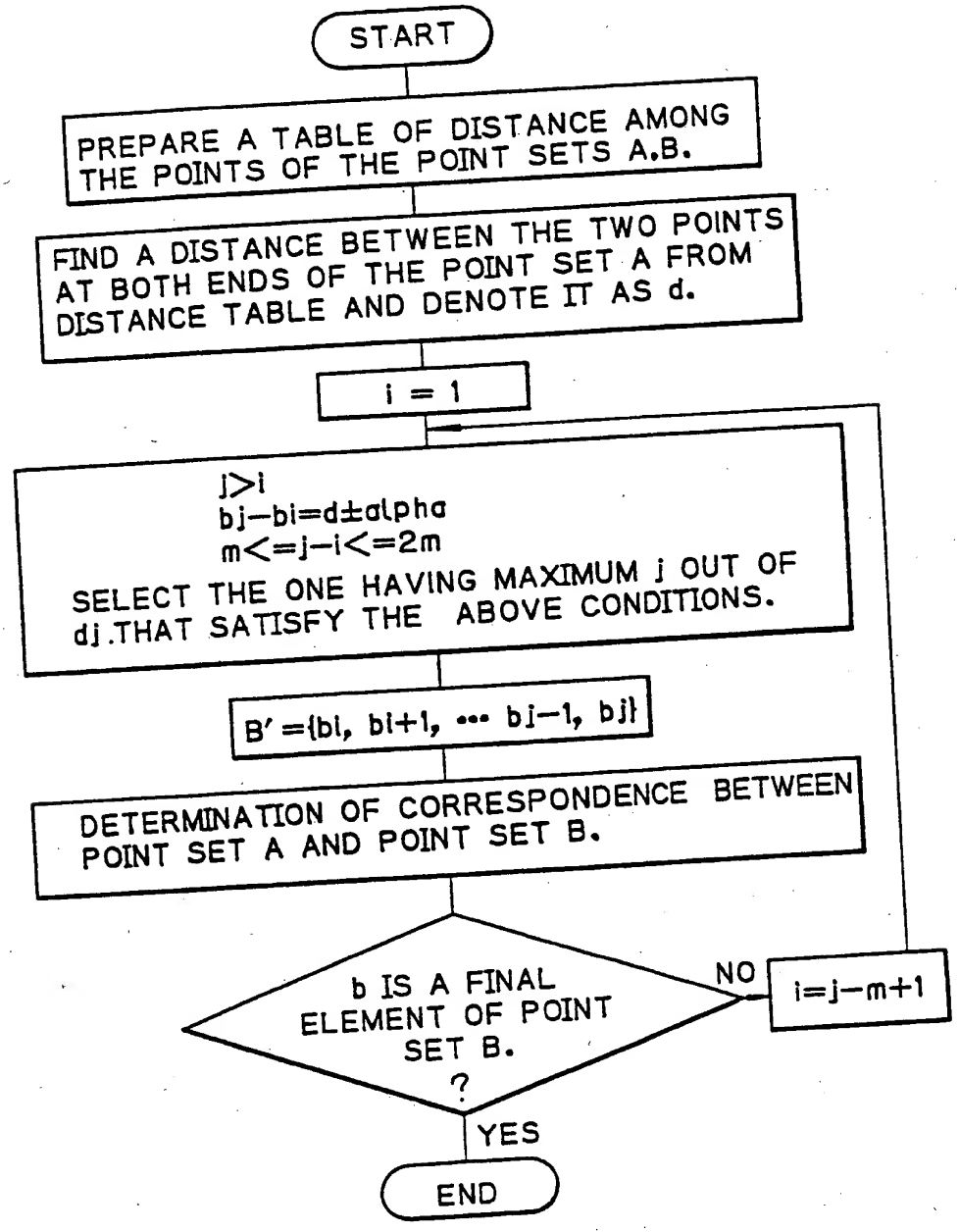


Fig. 38 A

1	I	V	G	G	Y	T	C	C	A	N	T	V	P	Y	Q	V	S	L	N	S
21	G	Y	H	F	C	G	G	S	L	I	N	S	Q	W	V	V	S	A	A	H
41	C	Y	K	S	G	I	Q	V	R	L	G	E	D	N	I	N	V	V	E	G
61	N	E	Q	F	I	S	A	S	K	S	I	V	H	P	S	Y	N	S	N	T
81	L	N	N	D	I	M	L	I	K	L	K	S	A	A	S	L	N	S	R	V
101	A	S	I	S	L	P	T	S	C	A	S	A	G	T	Q	C	L	I	S	G
121	W	G	N	T	K	S	S	G	T	S	Y	P	D	V	L	K	C	L	K	A
141	P	I	L	S	D	S	S	C	K	S	A	Y	P	G	Q	I	T	S	N	M
161	F	C	A	G	Y	L	E	G	G	K	D	S	C	Q	G	D	S	G	G	P
181	V	V	C	S	G	K	L	Q	G	I	V	S	W	G	S	G	C	A	Q	K
201	N	K	P	G	V	Y	T	K	V	C	N	Y	V	S	W	I	K	Q	T	I
221	A	S	N																	

SEQ ID NO: 14

AMINO ACID SEQUENCE OF TRYPSIN (EXCERPT FROM PDB)

Fig. 38 B

1	V	V	G	G	T	E	A	Q	R	N	S	W	P	S	Q	I	S	L	Q	Y
21	R	S	G	S	S	W	A	H	T	C	G	G	T	L	I	R	Q	N	W	V
41	M	T	A	A	H	C	V	D	R	E	L	T	F	R	V	V	V	G	E	H
61	N	L	N	Q	N	N	G	T	E	Q	Y	V	G	V	Q	K	I	V	V	
81	P	Y	W	N	T	D	D	V	A	A	G	Y	D	I	A	L	L	R	L	A
101	Q	S	V	T	L	N	S	Y	V	Q	L	G	V	L	P	R	A	G	T	I
121	L	A	N	S	P	C	Y	I	T	T	G	W	G	L	T	R	T	N	G	Q
141	L	A	Q	T	L	Q	Q	A	Y	L	P	T	V	D	Y	A	I	C	S	S
161	S	S	Y	W	G	S	T	V	K	N	S	M	V	C	A	G	G	D	G	V
181	R	S	G	C	Q	G	D	S	G	G	P	L	H	C	L	V	N	G	Q	Y
201	A	V	H	G	V	T	S	F	V	S	R	L	G	C	N	V	T	R	K	P
221	T	V	F	T	R	V	S	A	Y	I	S	W	I	N	N	V	I	A	S	N

SEQ ID NO: 15

AMINO ACID SEQUENCE OF ELASTASE (EXCERPT FROM PDB)

Fig. 39 A

```
Key site number 36 – 41 in Trypsin

41 42 43 44 45 46
 M  T  A  A  H  C    < target > SEQ ID NO: 16
 V  S  A  A  H  C    < probe  > SEQ ID NO: 17

d = 12.070038 [A]
r.m.s.d. = 0.061077 [A]
The number of atoms in a probe = 6
The number of atoms in PDB = 240
The number of combination = 1
Time = 1sec
```

RETRIEVED RESULTS OF HISTIDINE ACTIVE SITES

Fig. 39 B

```
Key site number 175 – 179 in Trypsin

186 187 188 189 190
  G   D   S   G   G   < target > SEQ ID NO: 18
  G   D   S   G   G   < probe  > SEQ ID NO: 19

d = 8.922721 [A]
r.m.s.d. = 0.092879 [A]
The number of atoms in a probe = 5
The number of atoms in PDB = 240
The number of combination = 1
Time = 1sec
```

RETRIEVED RESULTS OF SERINE ACTIVE SITES

Fig. 40

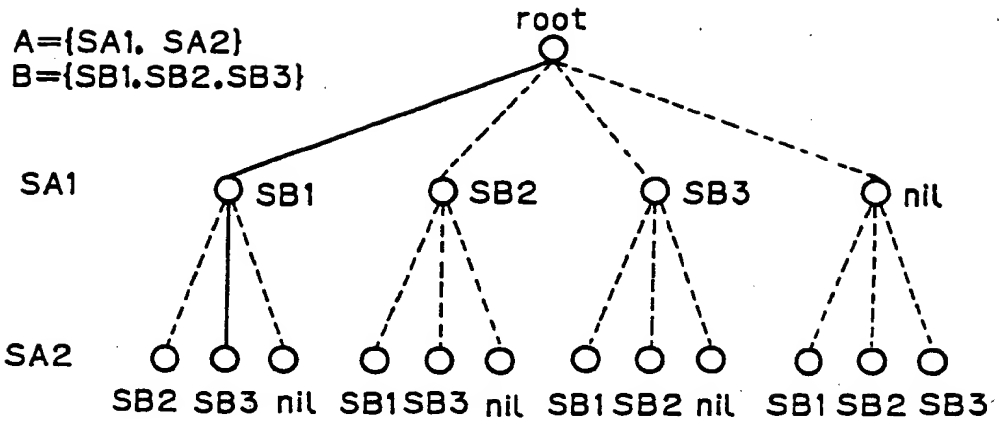


Fig. 41

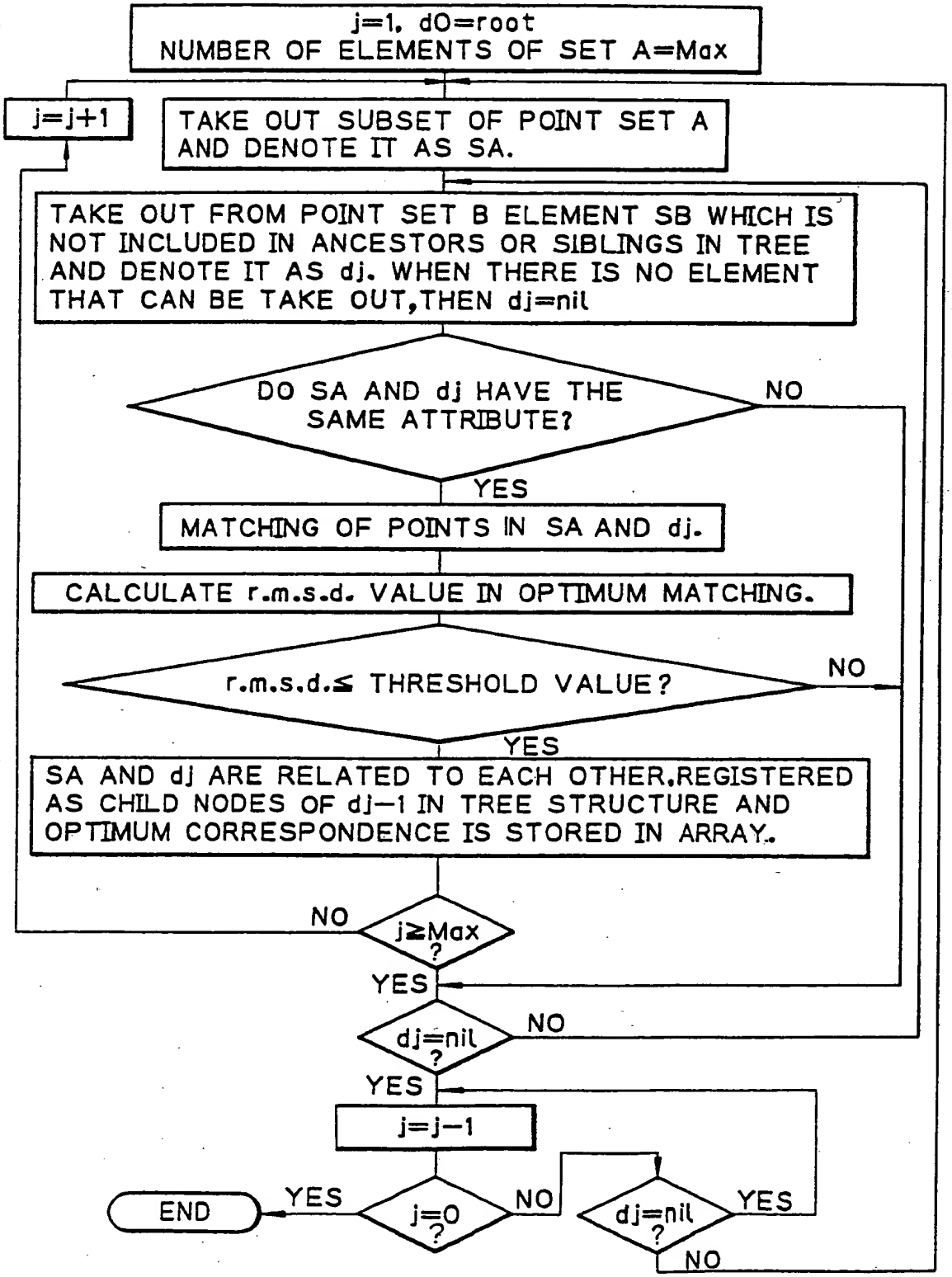


Fig. 42

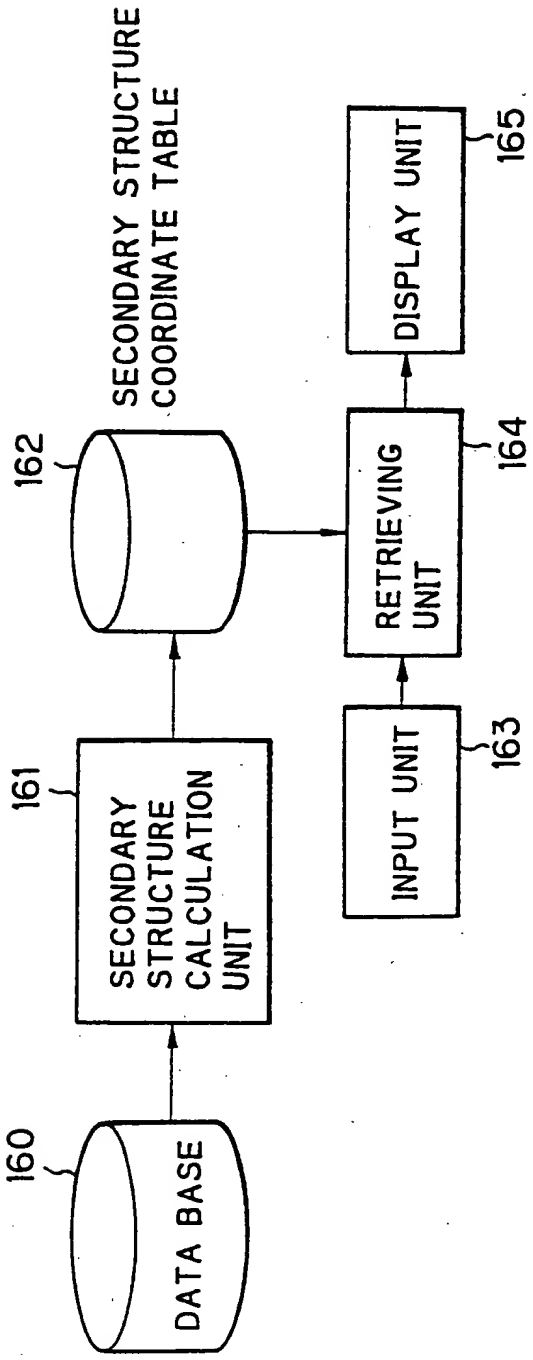


Fig. 43

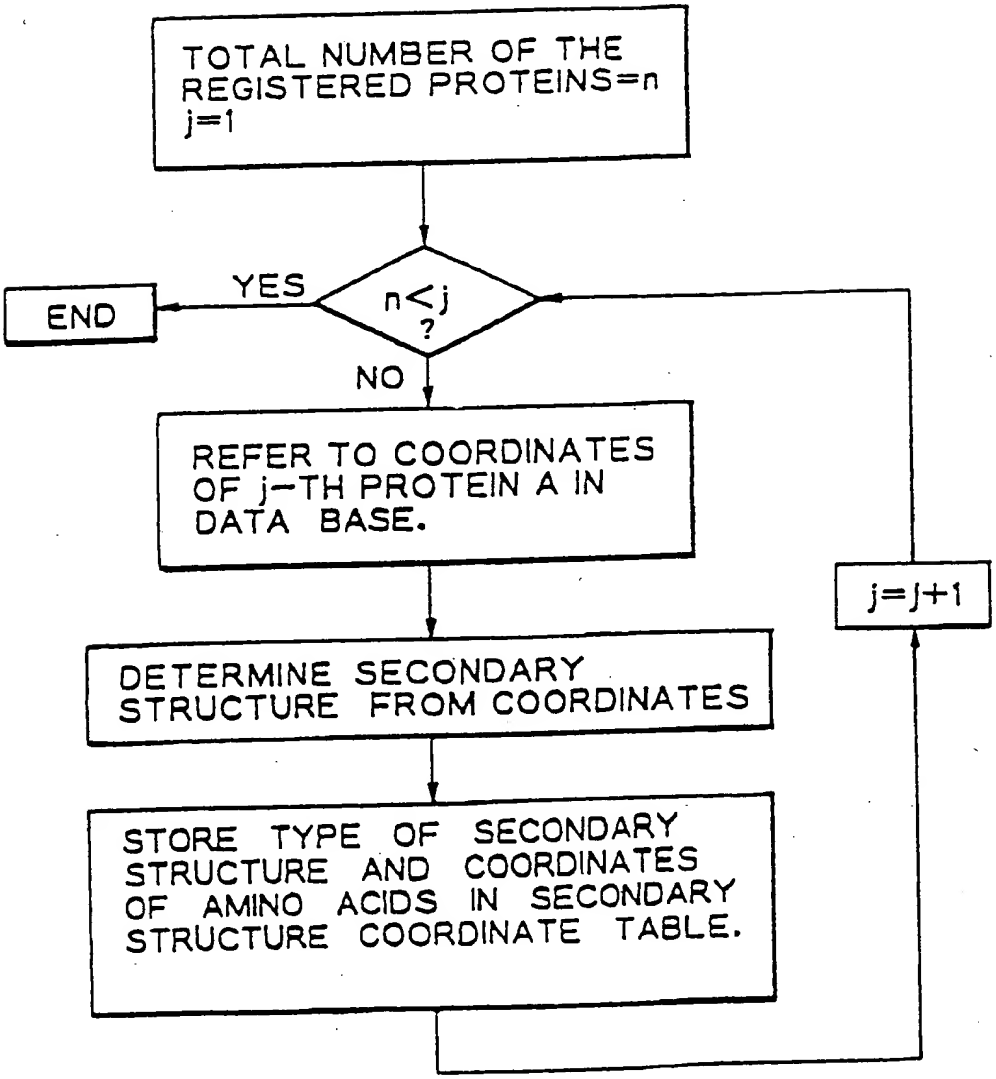


Fig. 44

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SUBSET	COORDINATES	TYPE
S1	{X1, X2, X3, X4, ····· Xa}	α — HELIX
S2	{Xa+1, Xa+2, ····· Xb}	α — HELIX
S3	{Xb+1, Xb+2, ····· Xc}	β — SHEET
S4	{Xc+1, Xc+2, ····· Xd}	β — SHEET
	⋮	⋮
Sn	{Xl+1, Xl+2, ····· Xm}	3 — TURN

Fig. 45

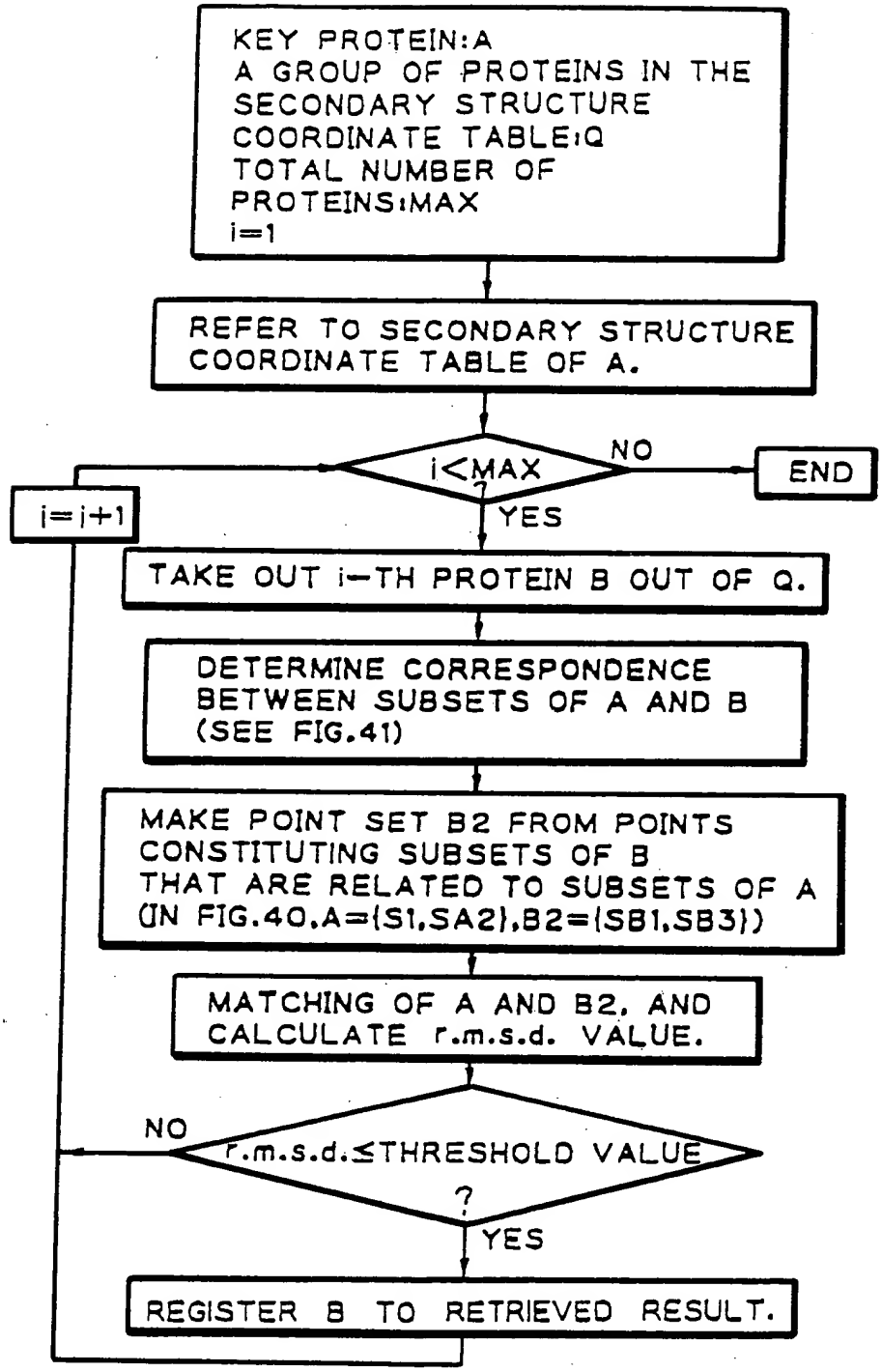
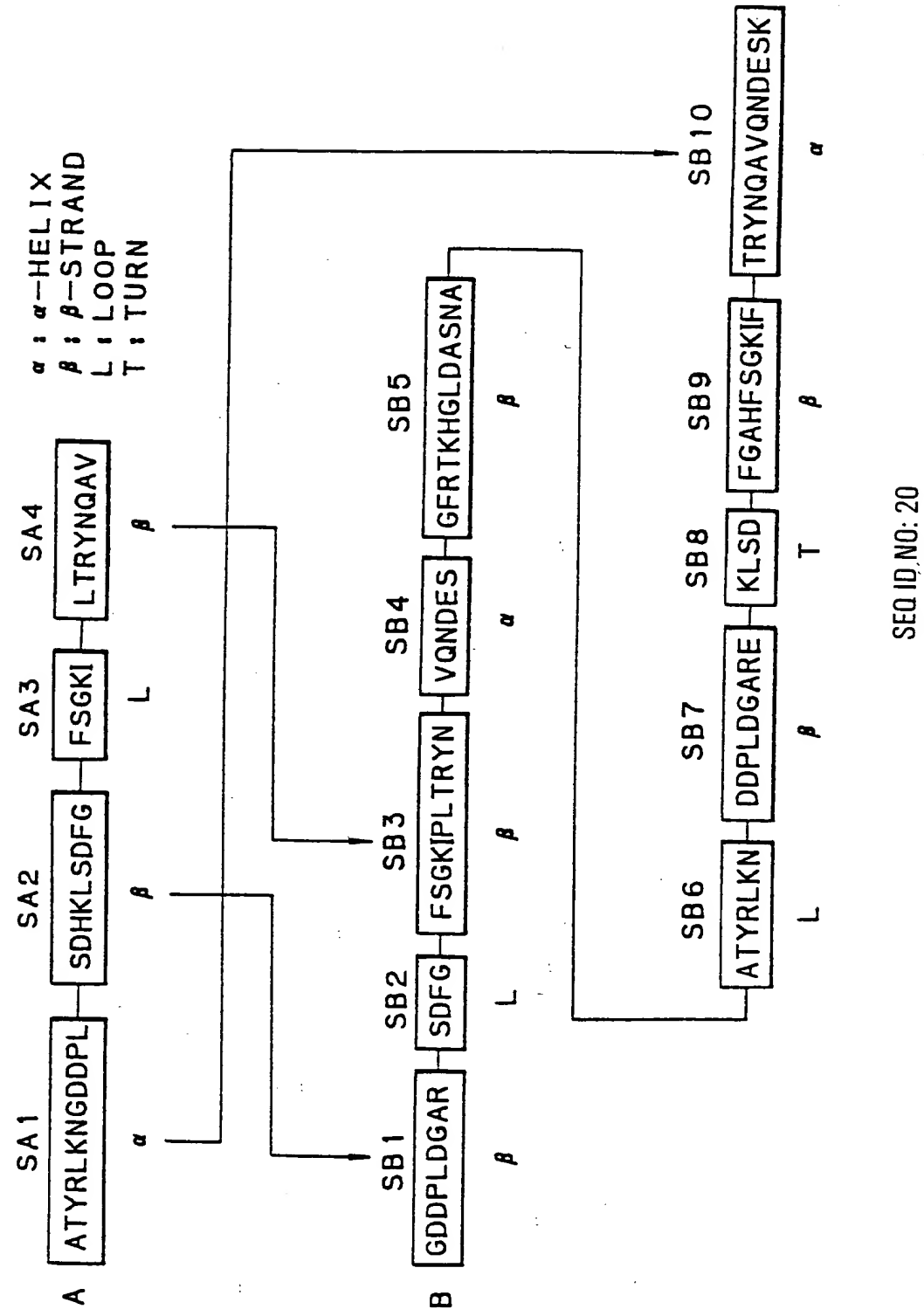
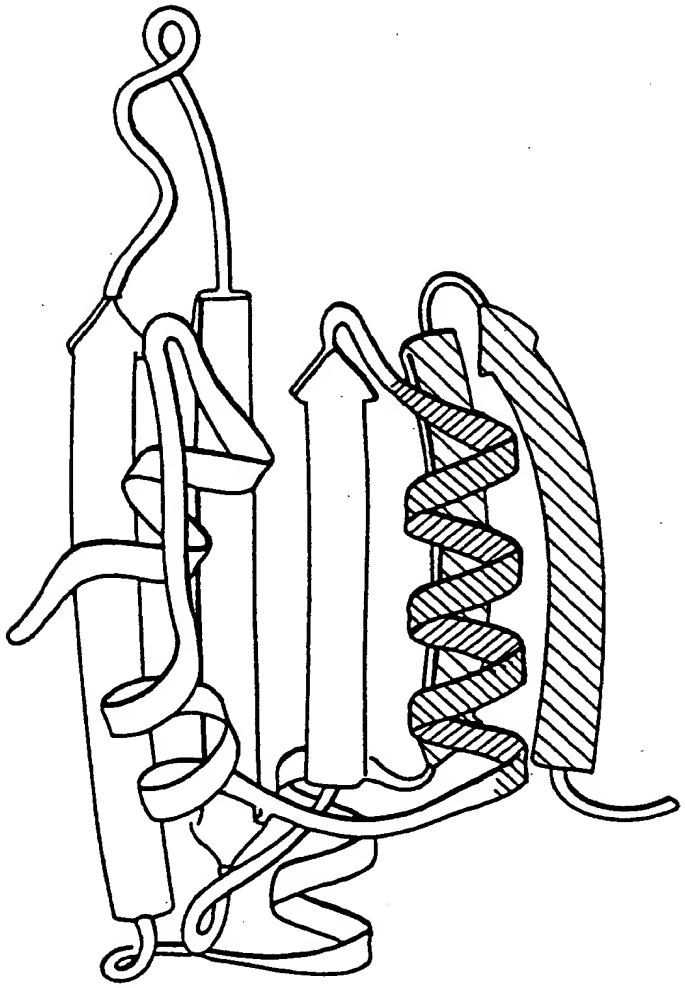


Fig. 46



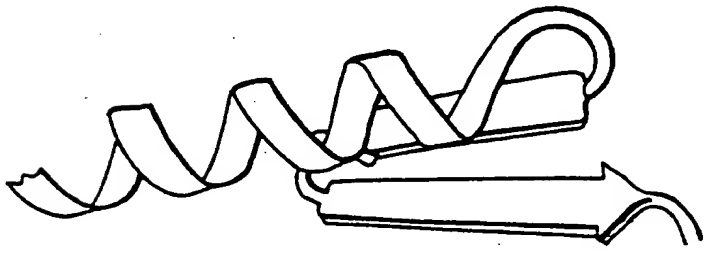
SEQ ID NO: 20

Fig. 47 B



PROTEIN B HAVING A SIMILAR STRUCTURE

Fig. 47 A



KEY PROTEIN A